



ClustalW Results

Sequences Help

Retrieved BLAST2 FASTA ClustalW GCG Assembly Phlip Translation

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☐ GSEB_AA55751
☐ 103561CD1

CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: GSEB_AA55751 2039 aa
Sequence 2: 103561CD1 174 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 66
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences: 2 Score:1942
Alignment Score 710
CLUSTAL-Alignment file created [baarka4ll.aln]
CLUSTAL W (1.7) Multiple sequence alignment

```
GSEB_AA55751      MGASSPRSPVPVGPAPGLPCCGSLAVVLLALPVAMGQNAPEMLPFARPTNLMD
103561CD1          -----MAPVRLERPFRPRLPGLLAALVLLSSPDCVPEMLPFARPTNLMD
* * * * *
GSEB_AA55751      PEPPIGYLAVRCRQVSGRPSTICLNKSVTGAADRCRKSQRNPDVNGMAYVIG
103561CD1          PEPPIGYLAVRCRQVSGRPSTICLNKSVTGAADRCRKSQRNPDVNGMAYVIG
* * * * *
GSEB_AA55751      IOPGQIKVSCCTGAYRLIGSSANCIISGDTVWENRPICDRIPOGLPPTITNGDPIST
103561CD1      IOPGQIKVSCCTGAYRLIGSSANCIISGDTVWENRPICDRIPOGLPPTITNGDPIST
* * * * *
GSEB_AA55751      NENPHYGSVVVYTRCNPGSGRKPVELVGEPSIYCTSNDDVGVWGSAPQCIIIPKCTP
103561CD1      L-----
GSEB_AA55751      PAVENGILVSDNRSLFSLAEVVEFRQCPGFVMEGPRRVKQALAKKWEPELPSCSRVCOP
103561CD1      PAVENGILVSDNRSLFSLAEVVEFRQCPGFVMEGPRRVKQALAKKWEPELPSCSRVCOP
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GSEB_AA55751      PVLHAERTORDKDNFSPGQEVVYSCPEGYDLGAASNAICTPOGDWSPAAPTCENKSCD
103561CD1      PVLHAERTORDKDNFSPGQEVVYSCPEGYDLGAASNAICTPOGDWSPAAPTCENKSCD
-----
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GSEB_AA55751      FMGQLNGRVLFPVNLQGAKVDPVCDEGFLQKGSASVYCLAAGMSLMSNVVCEQIF
103561CD1      -----
GSEB_AA55751      CPSPEVLPNGRHTGKPLEVPFGKAVNYTCDPIHPDRGTSFDLIGESTIRCTSDPQNGW
103561CD1      -----
GSEB_AA55751      SSPAPRCGILGHCOAPOHPLFAXLKTQTNASDPPIGTSIAKYECRPRYGRPFSTYCLNDL
103561CD1      -----
GSEB_AA55751      VMSSEKDVCKRKSCTPPDPVNGMAYVITMDIQGSRINYSCTTGHRLLGHSSAECTLSGN
103561CD1      -----
GSEB_AA55751      AAHNSRPPICORIPCGLPPTIANGDPISTNRNENPHYGSVVVYTRCNPGSGRKPVELVGE
103561CD1      -----
GSEB_AA55751      PSTVCTSNDDQVGIWGSAPQCIIIPKCTPNTENGILVSDNRSLFSLAEVVEFRQCPGF
103561CD1      -----
GSEB_AA55751      VNKGPBRVVKQALAKKWEPELPSCSRVCOPPDVLAERTORDKNFSPQGEVYSCPEGY
103561CD1      -----
GSEB_AA55751      DLRGASMRCTPQGDWSPAAPTCENKSCDPMGQLNGRVLFPVNLQGAKVDPVCDEG
103561CD1      -----
GSEB_AA55751      QLKGSASVYCLAAGMSLMSNVVCEQIFCPSPEVLPNGRHTGKPLEVPFGKAVNYTC
103561CD1      -----
GSEB_AA55751      DHPDRTGTSFDLIGESTIRCTSDPQNGWMSPAAPRCGILGHCOAPOHPLFAXLKTQTN
103561CD1      -----
GSEB_AA55751      SDPPIGSLKYECRPEVYGRPFSTICLDNLWMSSPEDVCKRKSCTPPDPVNGMAYVITD
103561CD1      -----
GSEB_AA55751      IQVGSRTNYSCTTGHRLLGHSSAECTLSGNTAMSTRPICORIPCGLPPTIANGDPIST
103561CD1      -----
GSEB_AA55751      NENPHYGSVVVYTRCNPGSGRKPVELVGEPSIYCTSNDDVGVWGSAPQCIIIPKCTP
103561CD1      -----
GSEB_AA55751      PAVENGILVSDNRSLFSLAEVVEFRQCPGFVMEGPRRVKQALAKKWEPELPSCSRVCOP
103561CD1      -----
GSEB_AA55751      PELHGERTPSHQDNFSPGQEVVYSCPEGYDLGAASNAICTPOGDWSPAAPTCENKSCD
103561CD1      -----
GSEB_AA55751      FLGQLPHGRVLFPVNLQGAKVDPVCDEGFLQKGSASVYCLAAGMSLMSNVVCEHIF
103561CD1      -----
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GSBQ_AAV5751 103561CD1	CPNPAILNGRHGTGSPSDIPYKKEISYTCDPHPDRGMTFNLIIGESTIRCTSDPHNGWV -----
GSBQ_AAV5751 103561CD1	SSPAPRCELSTVRAGHCKTPPEQPPASPTIPIINDEEPVGTSLNTECRDQYFGKMSISCL -----
GSBQ_AAV5751 103561CD1	ENLVMSIVEDNCRKSCGPPPEPFGNVAHINTDQFGSTVWVSCNEGFRLLIGSPSTCYL -----
GSBQ_AAV5751 103561CD1	SGNNVTMDKKAPICELIISCEPPPTISNGDPYSNNRTSPFNCTVTVYQCHTGPDEQLFEL -----
GSBQ_AAV5751 103561CD1	VGBRSIYCTSKDQVWVWSSPPRCISTNKCTAPEVENAIIVPQNSPFSULTELIIRRCQ -----
GSBQ_AAV5751 103561CD1	PGFVWVSGHTVQCQTNGRMGFKLPHCRAVCQPPPEILLGHEHTLSHDNFSFGQEVFYSCE -----
GSBQ_AAV5751 103561CD1	PSYDLRGAASLHCTPQGDWSEPAFRCTVYSCDDELQQLPHGRVLLPLANQLGAKVSPVCD -----
GSBQ_AAV5751 103561CD1	BGRRLKGRSASHCVLAGKALMNSVIVCEQIFCPNPAILNGRHGTGPGDIYKKEIS -----
GSBQ_AAV5751 103561CD1	YACDHPDRGTFENLIGESSIRCTSDPQNGWVSSPAPRCELSTVPAACPHPEKIQNGHYI -----
GSBQ_AAV5751 103561CD1	GGHVSILYLPGMTISYTCDPGYLLVGRGFIPTCTDQGIWSOLDHYCKEVNCSPLFMNGISK -----
GSBQ_AAV5751 103561CD1	ELBEMKVVHRGDIYVTLKCEGVTLESGFMSQCADDRMDPLACSTRADALIVGTLSG -----
GSBQ_AAV5751 103561CD1	TIFFILLIIFLSWILLKRRKGNNAHENPEVAIHLHSQGSVHPRTLQTNENSRLVP -----

Submit sequences to:





BLAST2 Search Results

Sequences Help

Retrieval BLAST2 FASTA ClustalW ICD Assembly Phrap Translation
BLAST2 Manual

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Program: blastp
Sequence ID(s):☐ 103561CD1 vs. Current: Geneseq_AA.fasta

NCBI-BLASTP 2.0.10 (Aug-26-1999)

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped Blast" and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 103561CD1
(174 letters)

Database: Current Geneseq_AA.fasta

1,029,157 sequences; 150,621,602 total letters

Searching.....done

Sequences producing significant alignments:

	Score	E
	(bits)	Value
<input checked="" type="checkbox"/> GSEQ:ABP64720 Human protein SEQ ID 380.	372	e-103
<input checked="" type="checkbox"/> GSEQ:AB68878 Human RECAP polypeptide, SEQ ID NO: 8.	372	e-103
<input checked="" type="checkbox"/> GSEQ:AAW75992 (CM16)-Cys-S-S-(MSMAP-1) polypeptide.	266	6e-71
<input checked="" type="checkbox"/> GSEQ:AAW75991 Complement receptor type 1-like polypeptide CM1	266	6e-71
<input checked="" type="checkbox"/> GSEQ:AAW75990 (CM15)-Cys-S-S-(MSMAP-1) polypeptide.	266	6e-71
<input checked="" type="checkbox"/> GSEQ:AAW75989 Complement receptor type 1-like polypeptide CM1	266	6e-71
<input checked="" type="checkbox"/> GSEQ:ABU11696 Human MDR1 polypeptide SEQ ID 643.	256	8e-68
<input checked="" type="checkbox"/> GSEQ:AAW50797 Human C3B/C4B receptor CR1 (complement receptor	256	8e-68
<input checked="" type="checkbox"/> GSEQ:AAW441010 Human polypeptide SEQ ID NO 5941.	256	8e-68
<input checked="" type="checkbox"/> GSEQ:AAW39224 Human polypeptide SEQ ID NO 2369.	256	8e-68
<input checked="" type="checkbox"/> GSEQ:ABB11782 Human CR1 protein homologue, SEQ ID NO:2152.	256	8e-68
<input checked="" type="checkbox"/> GSEQ:ABG00287 Novel human diagnostic protein #278.	256	8e-68
<input checked="" type="checkbox"/> GSEQ:AAW5751 Human C3b/C4b receptor (CR1) protein.	256	8e-68
<input checked="" type="checkbox"/> GSEQ:AAW73147 Amino acid sequence of the soluble complement x	256	8e-68
<input checked="" type="checkbox"/> GSEQ:AAW1810 Human complement type 1 receptor.	256	8e-68
<input checked="" type="checkbox"/> GSEQ:AAW2219 CR1 protein.	256	8e-68

<input checked="" type="checkbox"/> GSEQ:AAW28562 CR1-4 (116K) analogue.	253	7e-67
<input checked="" type="checkbox"/> GSEQ:AAW28552 CR1-4 (78F, 79D) analogue.	252	2e-66
<input checked="" type="checkbox"/> GSEQ:ABW26823 Membrane targeted complement inhibitor peptide.	251	2e-66
<input checked="" type="checkbox"/> GSEQ:ABW26817 Membrane targeted complement inhibitor peptide.	251	2e-66

>GSEQ:ABP64720 Human protein SEQ ID 380.
Length = 174Score = 372 bits (946), Expect = e-103
Identities = 174/174 (100%), Positives = 174/174 (100%)

Query: 1 MAPVRLERPPPSRRPFGLLAAVLVLLSFSPOCNVEMLPFAPFTNLTDDEPPIGRY 60
MAPVRLERPPPSRRPFGLLAAVLVLLSFSPOCNVEMLPFAPFTNLTDDEPPIGRY
Sbjct: 1 MAPVRLERPPPSRRPFGLLAAVLVLLSFSPOCNVEMLPFAPFTNLTDDEPPIGRY 60

Query: 61 LNTGCRPGVSGRPFSITICLNSVWTSADKCRKSCRNPPDPVNGAHVTKDIOFSQIR 120
LNTGCRPGVSGRPFSITICLNSVWTSADKCRKSCRNPPDPVNGAHVTKDIOFSQIR
Sbjct: 61 LNTGCRPGVSGRPFSITICLNSVWTSADKCRKSCRNPPDPVNGAHVTKDIOFSQIR 120

Query: 121 YSCPRGYRLIGSSATCIISGNTVIMDKTPVCDSELRVAFLELPHSNFSLE 174
YSCPRGYRLIGSSATCIISGNTVIMDKTPVCDSELRVAFLELPHSNFSLE
Sbjct: 121 YSCPRGYRLIGSSATCIISGNTVIMDKTPVCDSELRVAFLELPHSNFSLE 174

>GSEQ:ABW28562 Human RECAP polypeptide, SEQ ID NO: 8.
Length = 174Score = 372 bits (946), Expect = e-103
Identities = 174/174 (100%), Positives = 174/174 (100%)

Query: 1 MAPVRLERPPPSRRPFGLLAAVLVLLSFSPOCNVEMLPFAPFTNLTDDEPPIGRY 60
MAPVRLERPPPSRRPFGLLAAVLVLLSFSPOCNVEMLPFAPFTNLTDDEPPIGRY
Sbjct: 1 MAPVRLERPPPSRRPFGLLAAVLVLLSFSPOCNVEMLPFAPFTNLTDDEPPIGRY 60

Query: 61 LNTGCRPGVSGRPFSITICLNSVWTSADKCRKSCRNPPDPVNGAHVTKDIOFSQIR 120
LNTGCRPGVSGRPFSITICLNSVWTSADKCRKSCRNPPDPVNGAHVTKDIOFSQIR
Sbjct: 61 LNTGCRPGVSGRPFSITICLNSVWTSADKCRKSCRNPPDPVNGAHVTKDIOFSQIR 120

Query: 121 YSCPRGYRLIGSSATCIISGNTVIMDKTPVCDSELRVAFLELPHSNFSLE 174
YSCPRGYRLIGSSATCIISGNTVIMDKTPVCDSELRVAFLELPHSNFSLE
Sbjct: 121 YSCPRGYRLIGSSATCIISGNTVIMDKTPVCDSELRVAFLELPHSNFSLE 174

>GSEQ:AAW75992 (CM16)-Cys-S-S-(MSMAP-1) polypeptide.
Length = 215Score = 266 bits (674), Expect = 6e-71
Identities = 120/121 (99%), Positives = 120/121 (99%)

Query: 34 QCNVEMLPFAPFTNLTDDEPPIGTYLNTGCRPGVSGRPFSITICLNSVWTSADKCR 93
QCNVEMLPFAPFTNLTDDEPPIGTYLNTGCRPGVSGRPFSITICLNSVWTSADKCR
Sbjct: 2 QCNVEMLPFAPFTNLTDDEPPIGTYLNTGCRPGVSGRPFSITICLNSVWTSADKCR 61

Query: 94 KCCNPPDPVNGAHVTKDIOFSQIRKCRGRLIGSSATCIISGNTVIMDKTPVC 153
KCCNPPDPVNGAHVTKDIOFSQIRKCRGRLIGSSATCIISGNTVIMDKTPVC
Sbjct: 62 KCCNPPDPVNGAHVTKDIOFSQIRKCRGRLIGSSATCIISGNTVIMDKTPVC 121

Query: 154 D 154
D
Sbjct: 122 D 122

Score = 40.2 bits (92), Expect = 0.010
Identities = 38/144 (26%), Positives = 54/144 (37%), Gaps = 23/144 (15%)

Query: 29 SFSFQOC-----NVPEMLPFARPTNLTDPEFPIGYLYANECRPGY-----SGRPSIIC 78
+S D+C N P+ P ++ D +F + + Y C GY S II
Sbjct: 53 TSAKCKRKRKSCRNPPD--PVNGMAHVIKDIQFR--SQIKYSCRGYRLIGSSSACIIIS 108
Query: 79 LKNSVTSADKCKRSCRNPPDPVNGMAHYI--KDIQFSQIKYSCRGK-----YRLI 130
+W + C R C PP NG I + +GS + Y C G + L+
Sbjct: 109 GNTVIMDNKTPVCDRIICGLPPTIANGDFTSISREYFHGVSVYTHCNLGRKGFELV 168
Query: 131 GSSSATCIIISGNTV--IMDNKTPVC 153
G S C + V IW P C
Sbjct: 169 GEPSTYCTSKDQVGWISGPAQC 192

>GSEQ:AAW75991 Complement receptor type 1-like polypeptide CM16/cys.
Length = 198

Score = 266 bits (674), Expect = 6e-71
Identities = 120/121 (99%), Positives = 120/121 (99%)

Query: 34 QCNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 93
QCNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 61
Sbjct: 2 QCNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 61
Query: 94 KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGYRLIGSSSACIIISGNTVIMDNKTPVC 153
KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGYRLIGSSSACIIISGNTVIMDNKTPVC 121
Sbjct: 62 KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGYRLIGSSSACIIISGNTVIMDNKTPVC 121
Query: 154 D 154
D
Sbjct: 122 D 122

Score = 40.2 bits (92), Expect = 0.010
Identities = 38/144 (26%), Positives = 54/144 (37%), Gaps = 23/144 (15%)

Query: 29 SFSFQOC-----NVPEMLPFARPTNLTDPEFPIGYLYANECRPGY-----SGRPSIIC 78
+S D+C N P+ P ++ D +F + + Y C GY S II
Sbjct: 53 TSAKCKRKRKSCRNPPD--PVNGMAHVIKDIQFR--SQIKYSCRGYRLIGSSSACIIIS 108
Query: 79 LKNSVTSADKCKRSCRNPPDPVNGMAHYI--KDIQFSQIKYSCRGK-----YRLI 130
+W + C R C PP NG I + +GS + Y C G + L+
Sbjct: 109 GNTVIMDNKTPVCDRIICGLPPTIANGDFTSISREYFHGVSVYTHCNLGRKGFELV 168
Query: 131 GSSSATCIIISGNTV--IMDNKTPVC 153
G S C + V IW P C
Sbjct: 169 GEPSTYCTSKDQVGWISGPAQC 192

>GSEQ:AAW75990 (CM15)-Cys-S-(MSMAP-1) polypeptide.
Length = 215

Score = 266 bits (674), Expect = 6e-71
Identities = 120/121 (99%), Positives = 120/121 (99%)

Query: 34 QCNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 93
QCNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 61
Sbjct: 2 QCNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 61
Query: 94 KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGYRLIGSSSACIIISGNTVIMDNKTPVC 153
KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGYRLIGSSSACIIISGNTVIMDNKTPVC 121
Sbjct: 62 KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGYRLIGSSSACIIISGNTVIMDNKTPVC 121
Query: 154 D 154
D

Sbjct: 122 D 122

Score = 39.9 bits (91), Expect = 0.013
Identities = 38/144 (26%), Positives = 54/144 (37%), Gaps = 23/144 (15%)

Query: 29 SFSFQOC-----NVPEMLPFARPTNLTDPEFPIGYLYANECRPGY-----SGRPSIIC 78
+S D+C N P+ P ++ D +F + + Y C GY S II
Sbjct: 53 TSAKCKRKRKSCRNPPD--PVNGMAHVIKDIQFR--SQIKYSCRGYRLIGSSSACIIIS 108
Query: 79 LKNSVTSADKCKRSCRNPPDPVNGMAHYI--KDIQFSQIKYSCRGK-----YRLI 130
+W + C R C PP NG I + +GS + Y C G + L+
Sbjct: 109 GNTVIMDNKTPVCDRIICGLPPTIANGDFTSISREYFHGVSVYTHCNLGRKGFELV 168
Query: 131 GSSSATCIIISGNTV--IMDNKTPVC 153
G S C + V IW P C
Sbjct: 169 GEPSTYCTSKDQVGWISGPAQC 192

>GSEQ:AAW75989 Complement receptor type 1-like polypeptide CM15/cys.
Length = 198

Score = 266 bits (674), Expect = 6e-71
Identities = 120/121 (99%), Positives = 120/121 (99%)

Query: 34 QCNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 93
QCNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 61
Sbjct: 2 QCNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 61
Query: 94 KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGYRLIGSSSACIIISGNTVIMDNKTPVC 153
KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGYRLIGSSSACIIISGNTVIMDNKTPVC 121
Sbjct: 62 KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGYRLIGSSSACIIISGNTVIMDNKTPVC 121
Query: 154 D 154
D
Sbjct: 122 D 122

Score = 39.9 bits (91), Expect = 0.013
Identities = 38/144 (26%), Positives = 54/144 (37%), Gaps = 23/144 (15%)

Query: 29 SFSFQOC-----NVPEMLPFARPTNLTDPEFPIGYLYANECRPGY-----SGRPSIIC 78
+S D+C N P+ P ++ D +F + + Y C GY S II
Sbjct: 53 TSAKCKRKRKSCRNPPD--PVNGMAHVIKDIQFR--SQIKYSCRGYRLIGSSSACIIIS 108
Query: 79 LKNSVTSADKCKRSCRNPPDPVNGMAHYI--KDIQFSQIKYSCRGK-----YRLI 130
+W + C R C PP NG I + +GS + Y C G + L+
Sbjct: 109 GNTVIMDNKTPVCDRIICGLPPTIANGDFTSISREYFHGVSVYTHCNLGRKGFELV 168
Query: 131 GSSSATCIIISGNTV--IMDNKTPVC 153
G S C + V IW P C
Sbjct: 169 GEPSTYCTSKDQVGWISGPAQC 192

>GSEQ:ABU11696 Human MDOT polypeptide SEQ ID 643.
Length = 2044

Score = 256 bits (647), Expect = 8e-68
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLAALVLLLSFS--DQCNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPSI 76
G LLA +VLL + QCN VPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPSI 89
Sbjct: 30 GSLLAVVLLALPVAMQCNABEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPSI 89
Query: 77 ICLKNSVTSADKCKRSCRNPPDPVNGMAHYIKDIQFSQIKYSCRGYRLIGSSSAC 136

Query: 90 ICILNSWMT ARD-C-RKSCRNPPDPVNGM HV1K I0FSGQIKYSC KGRRLIGSSSAT
Sbjct: 137 CIIISGVTIMDKTPVCD 154
Query: 137 CIIISGVTIMDKTPVCD 154
Sbjct: 150 CIIISGVTIMDKTPVCD 167

Score = 176 bits (442), Expect = 9e-44
Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LSSFSIDQCNVPEMLPFARPTNLTDDEPPIGTIYLVNTECRPGYSGR-PFSITICLKNWTS 87
Sbjct: 1394 LSTRAGHKKTPPEOPFPAFTPIINDPEFVGSILNTECRPGYSGR-PFSITICLKNWTSV 1453

Query: 88 KDKCRKSCRNPPDPVNGMAHV1KDI0FSGQIKYSCPKGYRLIGSSSANCIIISGNTV1MD 147
Sbjct: 1454 EDNCRRKSCGPEPEPNMGVHINTDQFSGTVNSCNEGFRILGSPSTCLVSGNVTMD 1513

Query: 148 NKTTPVCD 154
Sbjct: 1514 KKAIPCE 1520

Score = 166 bits (417), Expect = 8e-41
Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 35 CNVPEMLPFARPTNLTDDEPPIGTIYLVNTECRPGYSGR-PFSITICLKNWTSADKCKRK 94
Sbjct: 948 COAPDHPFLFKLTQTNASDPPIGTSLKYECPREYGRPSITICLDNLVMSFKDCKRK 1007

Query: 95 SCRNPPDPVNGMAHV1KDI0FSGQIKYSCPKGYRLIGSSSANCIIISGNTV1MDKTPVCD 153
Sbjct: 1008 SCRTPEPVGMAHV1TIDQVGSINVSCTGTHLIGHSSAECILSGNAHNSKTPPIC 1066

Score = 164 bits (412), Expect = 3e-40
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNVPEMLPFARPTNLTDDEPPIGTIYLVNTECRPGYSGR-PFSITICLKNWTSADKCKRK 94
Sbjct: 498 COAPDHPFLFKLTQTNASDPPIGTSLKYECPREYGRPSITICLDNLVMSFKDCKRK 557

Query: 95 SCRNPPDPVNGMAHV1KDI0FSGQIKYSCPKGYRLIGSSSANCIIISGNTV1MDKTPVCD 153
Sbjct: 558 SCRTPEPVGMAHV1TIDQVGSINVSCTGTHLIGHSSAECILSGNAHNSKTPPIC 616

Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFSIDQCNVPEMLPFARPTNLTDDEPPIGTIYLVNTECRPGYSGR-PFSITICLKNWTS 86
Sbjct: 745 LPSGSRVQCPPEPDLHAERTQDND-NFSPQEVFVSCFEGYDLAGAASNRCTPGQWSP 803

Query: 87 AKDKCRKSCRNPPDPVNGMAHV1KDI0FSGQIKYSCPKGYRLIGSSSANCIIISGNTV1 145
Sbjct: 804 AAPTCVKSQCDPFGQLNGRVLPVNLQGLAKVDVCDGQQLKGSASVCLVAGMESTL 863

Query: 146 WDKTPVCD 154
Sbjct: 864 WNSVPVCE 872

Score = 68.7 bits (165), Expect = 3e-11

Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFSIDQCNVPEMLPFARPTNLTDDEPPIGTIYLVNTECRPGYSGR-PFSITICLKNWTS 86
Sbjct: 295 LPSGSRVQCPPEPDLHAERTQDND-NFSPQEVFVSCFEGYDLAGAASNRCTPGQWSP 353

Query: 87 AKDKCRKSCRNPPDPVNGMAHV1KDI0FSGQIKYSCPKGYRLIGSSSANCIIISGNTV1 145
Sbjct: 354 AAPTCVKSQCDPFGQLNGRVLPVNLQGLAKVDVCDGQQLKGSASVCLVAGMESTL 413

Query: 146 WDKTPVCD 154
Sbjct: 414 WNSVPVCE 422

Score = 64.8 bits (155), Expect = 4e-10
Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)

Query: 28 LSSFSIDQCNVPEMLPFARPTNLTDDEPPIGTIYLVNTECRPGYSGR-PFSITICLKNWTS 86
Sbjct: 1195 LPSGSRVQCPPEPDLHAERTSHQD-NFSPQEVFVSCFEGYDLAGAASNRCTPGQWSP 1253

Query: 87 AKDKCRKSCRNPPDPVNGMAHV1KDI0FSGQIKYSCPKGYRLIGSSSANCIIISGNTV1 145
Sbjct: 1254 EAPRCVASCDDPDLQPLPHGRVLPVNLQGLAKVSPVCDGFRILGSPSHCVLWGRSL 1313

Query: 146 WDKTPVCD 154
Sbjct: 1314 WNSVPVCE 1322

Score = 61.3 bits (146), Expect = 5e-09
Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)

Query: 49 LNDDEPPIGTIYLVNTECRPGYSGR-PFSITICLKNWTSADKCKRKSCRNPPDV-NGM 106
Sbjct: 1668 LSHQDNFSPQEVFVSCFEGYDLAGAASNRCTPGQWSP EAPRCVASCDDPDLQPLPHGR 1727

Query: 107 AHV1KDI0FSGQIKYSCPKGYRLIGSSSANCIIISGNTV1MDKTPVCD 154
Sbjct: 1728 VLLPMLNQLAKVSPVCDGFRILKRSASHCVLWGRSLWNSVPVCE 1775

Score = 48.0 bits (112), Expect = 5e-05
Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)

Query: 26 LLSFSIDQCNVPEMLPFARPTNLTDDEPPIGTIYLVNTECRPGYSGR-PFSITICL 79
Sbjct: 1448 LVMSVSVQCPPEPDLHAERTQDND-NFSPQEVFVSCFEGYDLAGAASNRCTPGQWSP 1504

Query: 80 ---KNSVTSADKCKRKSCRNPPDPVNGMAHV1KDI0FSGQIKYSCPKGYRLIGSSSANCIIISGNTV1 128
Sbjct: 1505 VSGNNVTSADKCKRKSCRNPPDPVNGMAHV1KDI0FSGQIKYSCPKGYRLIGSSSANCIIISGNTV1 1564

Query: 129 LIGSSSANCIIISGNTV1MDKTPVCD 158
Sbjct: 1565 LVGERSTVTSKDDQVWSPSPICSTYRK 1595

Score = 46.5 bits (108), Expect = 1e-04
Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)

Query: 57 IGVTLNTECRPGYSGR-PFSITICLKNWTSADKCKRKSCRNPPDV-NGM 110
Sbjct: 1736 LGARVSPVCDGFRILKRSASHCVLWGRSLWNSVPVCEQDTCRPAIILNGHRTPE 1795

Query: 111 KDIOGSOIKYSCPF-----KGYRLIGSSSATCII--SGNTVIMDKRTVPC 154
DI +G +I Y+C + LIG SS C GN V W + P C +
Sbjct: 1796 GDIPYKREISYACDHPHRCMTPLIGESIRCTSDPQNGV--WSPAPRC 1846

Score = 43.8 bits (101), Expect = 9e-04
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTVLANECRPGY---SGRPSTIIICLNKSWTSADKCKRSCNPPDPVNG--MAHYIK 111
G + Y C GY S II +W + C R C PP NG ++ +
Sbjct: 129 GSOIKYSCPKGRLIGSSSATCIIIGDPIVIMDKRTVPC 188

Query: 112 DIOGSOIKYSCPKG-----YRLIGSSSATCIIISGNTV--IMDKRTVPC 153
+GS + Y C G + L+G S C + + V IM P C
Sbjct: 189 NFHIGSVVTRCNPSGGRKVPYELVGPSTICTSDPQNGV--WSPAPRC 237

Score = 43.0 bits (99), Expect = 0.002
Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)

Query: 58 GTVLANECRPGY---SGRPSTIIICLNKSWTSADKCKRSCNPPDPVNG--MAHYIK 112
G + Y C GY G + F I C +W+ CR +C P +NG++ + K
Sbjct: 1875 GMTISYICDPGYLVNGKF--IPCTDQIWSQDLHCEKVCSPPLF--MNGISELEMKV 1932

Query: 113 IQGSOIKYSCPKGRLIGSSSATCIIISGNTVIMDKRTVPC 162
+G + C GY I GS + C S A +
Sbjct: 1933 YHGDVYTLKCEDFTLIGSPWOCQADR--NDPPLAKTSRAHMLI 1979

Score = 43.0 bits (99), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTYLANECRPGY---SGRPSTIIICLNKSWTSADKCKRSCNPPDPVNG--MAHYIK 107
+G+ +NY C G+ G + L + W++ C+R C PP NG ++
Sbjct: 575 DVOGSRINVSCTGHRILIGSSSATCIIISGNTVIMDKRTVPC 634

Query: 108 HYHIDIOGSOIKYSCPKG-----YRLIGSSSATCIIISGNTV--IMDKRTVPC 153
++GS + Y C G + L+G S C + + V IM P C
Sbjct: 635 TNRNHFHIGSVVTRCNPSGGRKVPYELVGPSTICTSDPQNGV--WSPAPRC 687

Score = 43.0 bits (99), Expect = 0.002
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGTVLANECRPGY---SGRPSTIIICLNKSWTSADKCKRSCNPPDPVNG--MAHYIK 110
+G+ +NY C G+ S ++ S+W ++ C+ C NP +NG
Sbjct: 1283 LGANVSFVCDGFRILIGSSSATCIIISGNTVIMDKRTVPC 1342

Query: 111 KDIOGSOIKYSCPF-----KGYRLIGSSSATCII--SGNTVIMDKRTVPC 158
DI +G +I Y+C + LIG SS C GN V W + P C +
Sbjct: 1343 GDIPYKREISYACDHPHRCMTPLIGESIRCTSDPQNGV--WSPAPRC 1397

Score = 42.6 bits (98), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTYLANECRPGY---SGRPSTIIICLNKSWTSADKCKRSCNPPDPVNG--MAHYIK 107
+G+ +NY C G+ S ++ S+W ++ C+ C NP +NG
Sbjct: 1023 DVOGSRINVSCTGHRILIGSSSATCIIISGNTVIMDKRTVPC 1084

Query: 108 HYHIDIOGSOIKYSCPKG-----YRLIGSSSATCIIISGNTV--IMDKRTVPC 153
++GS + Y C G + L+G S C + + V IM P C
Sbjct: 1085 TNRNHFHIGSVVTRCNPSGGRKVPYELVGPSTICTSDPQNGV--WSPAPRC 1137

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTVLANECRPGY---SGRPSTIIICLNKSWTSADKCKRSCNPPDPVNGMAHYIKD 112
+G +NY C G+ S ++ S+W S+ C++ C +PP NG H K
Sbjct: 383 LGANVDFVCDGFRILIGSSSATCIIISGNTVIMDKRTVPC 441

Query: 113 IQGSOIKYSCPF-----KGYRLIGSSSATCII--SGNTVIMDKRTVPC 153
++ FG + Y+C + LIG S+ C GN V W + P C
Sbjct: 442 LEVPEFGKAVNTDHPHRCMTPLIGESIRCTSDPQNGV--WSPAPRC 492

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTVLANECRPGY---SGRPSTIIICLNKSWTSADKCKRSCNPPDPVNGMAHYIKD 112
+G +NY C G+ S ++ S+W S+ C++ C +PP NG H K
Sbjct: 833 LGANVDFVCDGFRILIGSSSATCIIISGNTVIMDKRTVPC 891

Query: 113 IQGSOIKYSCPF-----KGYRLIGSSSATCII--SGNTVIMDKRTVPC 153
++ FG + Y+C + LIG S+ C GN V W + P C
Sbjct: 892 LEVPEFGKAVNTDHPHRCMTPLIGESIRCTSDPQNGV--WSPAPRC 942

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPAPFNLMDP-----EPIGTYLANECRPGYSGRP-----STICLNK-- 81
+P LP PT DF F G+ + Y C PG GR SI C N
Sbjct: 619 IPCLP-----PTIANGDFISTNRNHFHIGSVVTRCNPSGGRKVPYELVGPSTICTSDND 675

Query: 82 --SWTSADKCKRSCNPPDPVNGMAHYIKD-----IQGSOIKYSCPKGRLIGSSSA 135
+W+ +C + PP+ NG+ ++ D +++ C G+ + G
Sbjct: 676 QVGWISGAPACIIPNKCPTPVNENG--LVSDNLSLFLSINEVVERFQCPVMAKGRPV 733

Query: 136 NCIIISGNTVIMDKRTVPC 153
C W+ + P C
Sbjct: 734 KQALNK--WEPELPSC 748

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPAPFNLMDP-----EPIGTYLANECRPGYSGRP-----STICLNK-- 81
+P LP PT DF F G+ + Y C PG GR SI C N
Sbjct: 169 IPCLP-----PTIANGDFISTNRNHFHIGSVVTRCNPSGGRKVPYELVGPSTICTSDND 225

Query: 82 --SWTSADKCKRSCNPPDPVNGMAHYIKD-----IQGSOIKYSCPKGRLIGSSSA 135
+W+ +C + PP+ NG+ ++ D +++ C G+ + G
Sbjct: 226 QVGWISGAPACIIPNKCPTPVNENG--LVSDNLSLFLSINEVVERFQCPVMAKGRPV 283

Query: 136 NCIIISGNTVIMDKRTVPC 153
C W+ + P C
Sbjct: 284 KQALNK--WEPELPSC 298

Score = 36.4 bits (82), Expect = 0.15
Identities = 33/117 (28%), Positives = 45/117 (38%), Gaps = 21/117 (17%)

Query: 54 EPIGTYLANECRPGY---SGRPSTIIICLNKSWTSADKCKRSCNPPDPVNG--MAHYIK 99
+P G +NY C G +P+I C N W+ S +C+ +C +P
Sbjct: 1797 DIPYKREISYACDHPHRCMTPLIGESIRCTSDPQNGV--WSPAPRC 1856

P NG HV + G I Y C GY L+G C G IW C
Sbjct: 1857 EKIQNGHYIGGNVSLYLP-GMTISTYICDPGYLLVNGKGIIFCTOG---INSQLDHYC 1909

Score = 36.4 bits (82), Expect = 0.15
Identities = 33/128 (25%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PNLNLDLP-----EPIGTYLNEYCRPGYSGRPF-----SIICLNK---SWTSAK 88
PT DF F GR + Y+C G G SI C VM+S

Sbjct: 1528 PTISMDGFYSNNRSTFNGVTVTYQCHTQDGBQLPELVGRSITCYCTSKDQGVWSSPF 1587

Query: 89 DKCRKRSKRNPDVPNGMAHVIKDIQFGSQIKYSCPKGYRLIGSSATCIISGNVTI 145
+C +C +F+ N + V + F S +++ C G+ +GS + C +G
Sbjct: 1588 FPGISTKCTAPEVENAI-RVGRNSPFSULTEIVRRCQPGFVAGSHVOCQTNR--- 1643

Query: 146 WDKRTPVC 153
W K P C

Sbjct: 1644 WGFKLPHC 1651

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPNLTDPEPPIGTYLNEYCRPGYS-GRPSIIT-----CLK---NSV 83
C P +P R T + PP G +NY C P G F +I C N V

Sbjct: 426 CPSPVITNGRHNGKPLEV-FPEKTVNTCDPHDRGTSPDLIGESTIICSDPOANGV 484

Query: 84 WTSADKCK-RKSCRNPDVPNGMAHV---IKDIQFGSQIKYSCPKGYRLIGSSATCI 139
W+S +C C+ P + D G+ +KY C Y S TC+

Sbjct: 485 WSSPAPRCGILGHCOAHDHFLPAKLKQTNASDPPIGTSLKYECPREY-YGRPSITCL- 542

Query: 140 SGNVTIWDKRTVC 153
+ + +W + VC

Sbjct: 543 --DNLVWSSPFDVC 554

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPNLTDPEPPIGTYLNEYCRPGYS-GRPSIIT-----CLK---NSV 83
C P +P R T + PP G +NY C P G F +I C N V

Sbjct: 876 CPSPVITNGRHNGKPLEV-FPEKTVNTCDPHDRGTSPDLIGESTIICSDPOANGV 934

Query: 84 WTSADKCK-RKSCRNPDVPNGMAHV---IKDIQFGSQIKYSCPKGYRLIGSSATCI 139
W+S +C C+ P + D G+ +KY C Y S TC+

Sbjct: 935 WSSPAPRCGILGHCOAHDHFLPAKLKQTNASDPPIGTSLKYECPREY-YGRPSITCL- 992

Query: 140 SGNVTIWDKRTVC 153
+ + +W + VC

Sbjct: 993 --DNLVWSSPFDVC 1004

>GSEB_LAM50797 Human C3B/C4B receptor CRL (complement receptor type 1).
Length = 2039

Score = 256 bits (647), Expect = 8e-68
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLAALVLLSSFS--DOCNPEMLPFARPNLTDPEPPIGTYLNEYCRPGYSGRPSI 76
G IIA +YL + OCN PEMLPFARPNLTDPEPPIGTYLNEYCRPGYSGRPSI

Sbjct: 25 GSLLAVVLLALVPMWGQCNPEMLPFARPNLTDPEPPIGTYLNEYCRPGYSGRPSI 84

Query: 77 ICLKNSVWTAKDKCRKRSKRNPDVPNGMAHVIKDIQFGSQIKYSCPKGYRLIGSSAT 136
ICLKNSVWT AKD+C+RKSCRNPDVPNGM HVIK IQFGSQIKYSC KGYRLIGSSAT

Sbjct: 85 ICLKNSVWTAKDKCRKRSKRNPDVPNGMAHVIKDIQFGSQIKYSCPKGYRLIGSSAT 144

Query: 137 CIISG+TVINDN-TP+CD 154
CIISG+TVINDN-TP+CD

Sbjct: 145 CIISGDTVIMDNETPICD 162

Score = 176 bits (442), Expect = 9e-44
Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LSSFDQCNVPEMLPFARPNLTDPEPPIGTYLNEYCRPGYSGRPSIICLNKNSVWTS 87
LS + C PE PFA PT +DEEP+CT LNEYCRPGY G+FSI CLAN VM+S

Sbjct: 1389 LSVYAGHCTPEQPPFASPTIPIANDPEPPIGTYLNEYCRPGYSGRPSIICLNKNSV 1448

Query: 88 KDKCRKRSKRNPDVPNGMAHVIKDIQFGSQIKYSCPKGYRLIGSSATCIISGNVTI 147
+D C+RKSC PP+P NGM H+ D QFGS + YSC +G+RLIGS S TC++SGN V WD

Sbjct: 1449 EDNCRKRSKRNPDVPNGMAHVINTDQFGSTVWYSCNGBRLIGSPSTYLVAGNNVTMD 1508

Query: 148 NKRTVCD 154
K P+C+

Sbjct: 1509 KKAIPCE 1515

Score = 166 bits (417), Expect = 8e-41
Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 35 CNVPEMLPFARPNLTDPEPPIGTYLNEYCRPGYSGRPSIICLNKNSVWTSADKCKR 94
C P+ FA+ T+ +PIGT L YECRP Y GRPSI CL N VM+S KD CKR

Sbjct: 943 COADPHFLPAKLKQTNASDPPIGTSLKYECPREYGRPSITCLDNLVWSSPFDVC 1002

Query: 95 SCRNPDVPNGMAHVIKDIQFGSQIKYSCPKGYRLIGSSATCIISGNVTIWDKRTVC 153
SC+ PPDVNGM HVI DIQ GS+I YSC G+RLIG SSA CI+SGN W K P+C

Sbjct: 1003 SCRTPEPVPNGMAHVITDIQVGRINYSCTGHRLLIGHSSACILSGNFAHMTKPEIC 1061

Score = 164 bits (412), Expect = 3e-40
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNVPEMLPFARPNLTDPEPPIGTYLNEYCRPGYSGRPSIICLNKNSVWTSADKCKR 94
C P+ FA+ T+ +PIGT L YECRP Y GRPSI CL N VM+S KD CKR

Sbjct: 493 COADPHFLPAKLKQTNASDPPIGTSLKYECPREYGRPSITCLDNLVWSSPFDVC 552

Query: 95 SCRNPDVPNGMAHVIKDIQFGSQIKYSCPKGYRLIGSSATCIISGNVTIWDKRTVC 153
SC+ PPDVNGM HVI DIQ GS+I YSC G+RLIG SSA CI+SGN W K P+C

Sbjct: 553 SCRTPEPVPNGMAHVITDIQVGRINYSCTGHRLLIGHSSACILSGNFAHMTKPEIC 611

Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFDQCNVPEMLPFARPNLTDPEPPIGTYLNEYCRPGYSGRPSIICLNKNSVWTS 86
L S S C P + A T D P G + Y C RY R S+ C W+

Sbjct: 740 LPSCSNVCPPEPVLHAERTORDK-NFSQDEYFISCEPGLDAGNASHCTPOGMSF 798

Query: 87 AKDKCRKRSKRN-PDVPNGMAHVIKDIQFGSQIKYSCPKGYRLIGSSATCIISGNVTI 145
A C +KSC + +NG +Q G+++ + C +G+L GSS++ C++G +

Sbjct: 799 AAPTCEVSCDDMQILNGRVLPVNLQAKADVCEGFOLGKSSAYCVLAGEML 858

Query: 146 WDKRTPVC 154
W++ PVC+

Sbjct: 859 MNSSVPCE 867

Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFDQCNVPEMLPFARPTNLTDPEPIGTALNTECRPGYSR--PFSIIICLNKSWMTS 86
L S S C P + A T D P G + Y C PGY R S+ C W+
Sbjct: 290 LPSCSNVCOPEPVLHARTORD--NFSPOEVYSCPEPDLRGASLRCTPGQMSF 348
Query: 87 AKDKRKRSCRN--PDPVNGAHYIKDIQFSQIKYSCPKGYRLIGSSATCIISGNTV 145
A C KSC + NG +Q G+++ + C +G++L GSS+ C++ G +
Sbjct: 349 AATPEWAKSCDDPMQGLNGLRVLEPVLNQLAKATDPCVCEGQLKSSASVYLAAGESL 408
Query: 146 KDKKTPVCD 154
W+ PGC+
Sbjct: 409 WNSVPCVCE 417

Score = 64.8 bits (155), Expect = 4e-10
Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)

Query: 28 LSSFDQCNVPEMLPFARPTNLTDPEPIGTALNTECRPGYSR--PFSIIICLNKSWMTS 86
L S S C P + T D P G + Y C PGY R S+ C W+
Sbjct: 1190 LPSCSNVCOPEPVLHARTPHQD--NFSPOEVYSCPEPDLRGASLRCTPGQMSF 1248
Query: 87 AKDKRKRSCRN--PDPVNGAHYIKDIQFSQIKYSCPKGYRLIGSSATCIISGNTV 145
+ C KSC + +G +Q G+++ + C +G++L GSS + C++ G +
Sbjct: 1249 EAPFCAVSCDDPLGOLPHGRVLPFLNQLGAKAVSPVCEBGLKSSSVSHCVLAKMSL 1308
Query: 146 KDKKTPVCD 154
W+N PGC+
Sbjct: 1309 WNSVPCVCE 1317

Score = 61.3 bits (146), Expect = 5e-09
Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)

Query: 49 LTTDFEPIGTALNTECRPGYSR--PFSIIICLNKSWMTSADKCRKSCRNPDVNG--NGM 106
L+ S P G + Y C P Y R S+ C W+ +C KSC + +G
Sbjct: 1663 LSHDNFSPGOEVYSCPEPDLRGASLRCTPGQMSFEPKCDPLGOLPHGR 1722
Query: 107 AHVTKDIQFSQIKYSCPKGYRLIGSSATCIISGNTVIMDNKTPVCD 154
+ +Q G+++ + C +G++L G S++ C++G +W++ PGC+
Sbjct: 1723 VILPLNQLGAKAVSPVCEBGLKRSASHCVLAGKALMNSVPCVCE 1770

Score = 48.0 bits (112), Expect = 5e-05
Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)

Query: 26 LLLSFDQCNV---PEMLPFARPTNLTDPEPIGTALNTECRPGYS--GRPFSIIICL 79
L+ S S D C P P F ++ D +F G+ +NY C G+ G P S CL
Sbjct: 1443 LMSVSEVDCRKRKSCGPEPPEPFGVHINTDQF--GSTVNYSCNCGFRLLGSP--STICL 1499
Query: 80 ---KNSVWTSADKCRKSCRNPDVNGAHYIKDIQF--GSQIKYSCPKG-----YR 128
N W M C+ SC P NG + P G+ + Y C G +
Sbjct: 1500 VSGNNVWTKKAPICETIISCPEPPTISNDFYISNNRSTPHNGVTVYTCGHDGQGLFE 1559
Query: 129 LIGSSATCIISGNTV--IMDNKTPVCDSELK 158
L+G S C + V W+ + P C S K
Sbjct: 1560 LVGRSIVCTSKDQVGVWSSPPPCISTYK 1590

Score = 46.5 bits (108), Expect = 1e-04
Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)

Query: 57 IGTALNTECRPGY--SGRPFSS--ITCLAKSWMTSADKCRKSCRNPDVNG--MAHYI 110
+G +++ C G+ GR S ++ +W S+ C++ C NFP +NG
Sbjct: 1731 LGAVSPVCEBGLKRSASHCVLAGKALMNSVPCVCIQCPNPALLNGRHTGPF 1790

Query: 111 KDIOFSQIKYSCP-----KGYRLIGSSATCIIS--SGNTVIMDNKTPVCD 154
DI +G +I Y+C + LIG SS C GN V W + P C +
Sbjct: 1791 GDIVGEISYACDTHPDGKMTPLNIGESIRCTSDQNGNV--WSSPAFCE 1841
Score = 43.8 bits (101), Expect = 9e-04
Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)

Query: 58 GTYLANTECRPGYS--GRPFSIIICLNKSWMTSADKCRKSCRNPDVNG--MAHYI 112
G +Y C PGY G+ F I C +W+ CR +C P +NG++ + K
Sbjct: 1870 GATISTYCDPGLVWKGKF--IFCTDQIGMSQDHYCEVNCSPFLP--WNGISKELEKRV 1927
Query: 113 IQFSQIKYSCPKGYRLIGSSATCIISGNTVIMDNKTPVCDSELKAYFL 162
+G + C GY L GS + C WD C S A +
Sbjct: 1928 YHGDVYTLKCEDGYTLGSPWSCQADDR--MDPLAKTSSRAHDALI 1974

Score = 43.8 bits (101), Expect = 9e-04
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTYLANTECRPGY---SGRPFSSIIICLNKSWMTSADKCRKSCRNPDVNG--MAHYI 111
G+ + Y C GY S II +W+ C R C P NG ++ +
Sbjct: 124 GSOIYSCCTGYRLIGSSATCIISGNTVIMDNKTPVCDIPGCLPPTTGWDFISTNRE 183
Query: 112 DIQFSQIKYSCPKG-----YRLIGSSATCIISGNTV--IMDNKTPVCD 153
+ +GS + Y C G +L+G S C + + V IW P C
Sbjct: 184 NPHGSVTVYTRCNPGSGRKYFELVGEPSIYCTSDQVIGWISGPAFQC 232

Score = 43.0 bits (99), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTALNTECRPGYS--GRPFSIIICLNKSV--WTSADKCRKSCRNPDVNG--NA 107
+ +G+ +NY C G+ G + L + W++ C+R C P NG ++
Sbjct: 570 DIQVDSINISCTGHRILIGSSATCIISGNAHMASTPRLCQRIQGLPPTIANDGFIS 629
Query: 108 HVTKDIQFSQIKYSCPKG-----YRLIGSSATCIISGNTV--IMDNKTPVCD 153
++ +GS + Y C G +L+G S C + + V IW P C
Sbjct: 630 TTRNPHYSVTVYTRCNPGSGRKYFELVGEPSIYCTSDQVIGWISGPAFQC 682

Score = 43.0 bits (99), Expect = 0.002
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGTALNTECRPGY---SGRPFSSIIICLNKSWMTSADKCRKSCRNPDVNG--MAHYI 110
+G +++ C G+ S ++ S+W ++ C+ C NFP +NG
Sbjct: 1278 LGAKVSPVCEBGLKSSVSHCVLAGKALMNSVPCVCEHIFCENPALLNGRHTGPF 1337
Query: 111 KDIOFSQIKYSCP-----KGYRLIGSSATCIIS--GNVYIMDNKTPVCDSELK 158
DI +G +I Y+C + LIG S+ C GN V W + P C+ ++
Sbjct: 1338 GDIVGEISYCTDHPDGMTPNLIGESTICTSDPHNGNV--WSSPAFCELSYR 1392

Score = 42.6 bits (98), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTALNTECRPGYSGRPFS---ITCLAKSWMTSADKCRKSCRNPDVNG--MA 107
+G+ +NY C G+ S I+ + W++ C+R C P NG ++
Sbjct: 1020 DIQVDSINISCTGHRILIGSSATCIISGNAHMASTPRLCQRIQGLPPTIANDGFIS 1079
Query: 108 HVTKDIQFSQIKYSCMG-----YRLIGSSATCIISGNTV--IMDNKTPVCD 153
++ +GS + Y C G +L+G S C + + V IW P C
Sbjct: 1080 TTRNPHYSVTVYTRCNLGSGRKRYFELVGEPSIYCTSDQVIGWISGPAFQC 1132

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTLANEGRBY-----SGRPSITCLKNSWTSAKDKCRKSCNPPDPVNGMAHVKD 112
+G +++ C G+ S +++ S+W S+ C++ C +PP NG H K
Sbjct: 378 LQAKVDVCDGDFOLKGSASVCYVLAIGESLWSSVPCQDFCPSPVPIVNG-RHTGKP 436

Query: 113 IQ--FGSQIKYSCP-----KGYRLIGSSSANCII--SGNTVIMDKTTPVC 153
++ FG + Y+C + LIG S+ C GN V W + P C
Sbjct: 437 LEVFPFGKAVNYTCDPHDRGTSFDLIGESTRICTSDPGNGV-WSPAPRC 487

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTLANEGRBY-----SGRPSITCLKNSWTSAKDKCRKSCNPPDPVNGMAHVKD 112
+G +++ C G+ S +++ S+W S+ C++ C +PP NG H K
Sbjct: 828 LQAKVDVCDGDFOLKGSASVCYVLAIGESLWSSVPCQDFCPSPVPIVNG-RHTGKP 886

Query: 113 IQ--FGSQIKYSCP-----KGYRLIGSSSANCII--SGNTVIMDKTTPVC 153
++ FG + Y+C + LIG S+ C GN V W + P C
Sbjct: 887 LEVFPFGKAVNYTCDPHDRGTSFDLIGESTRICTSDPGNGV-WSPAPRC 937

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPBMLPFPAPFNLTDDP-----EPPIGYLANTECRPGYSGRPF-----STICLN-- 81
+P LP P P D P F G+ + Y C PG GR SI C N
Sbjct: 614 IPGGLP--PTIANGDFISTNENFHYGSAVYTRCNPSGGRKVELVGPSTICTSDND 670

Query: 82 --SWTSAKDKCRKSCNPPDPVNGMAHVKD----IQFGSQIKYSCPGRYRLIGSSSA 135
+W+ +C + PP+ NG+ ++ D +++ C G+ + G
Sbjct: 671 QVGWISGAPQCIIPNKCCTPPVANGI--LVSDNRSLFSLANEVFEFGQDFVNGPRPV 728

Query: 136 TCIIISGNTVIMDKTTPVC 153
C W+ + P C
Sbjct: 729 KCOALNR--WEPPLPSC 743

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPBMLPFPAPFNLTDDP-----EPPIGYLANTECRPGYSGRPF-----STICLN-- 81
+P LP P P D P F G+ + Y C PG GR SI C N
Sbjct: 164 IPGGLP--PTIANGDFISTNENFHYGSAVYTRCNPSGGRKVELVGPSTICTSDND 220

Query: 82 --SWTSAKDKCRKSCNPPDPVNGMAHVKD----IQFGSQIKYSCPGRYRLIGSSSA 135
+W+ +C + PP+ NG+ ++ D +++ C G+ + G
Sbjct: 221 QVGWISGAPQCIIPNKCCTPPVANGI--LVSDNRSLFSLANEVFEFGQDFVNGPRPV 278

Query: 136 TCIIISGNTVIMDKTTPVC 153
C W+ + P C
Sbjct: 279 KCOALNR--WEPPLPSC 293

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPIGYLANTECRPGYS-GRPSII-----CLK-----NSWTSAKDKCRK--SCNPP 99
+ P G ++Y C G P++I C N W+S ++C +P
Sbjct: 1792 DIPYGRKISYACDHPDRGTRNLIGESTRICTSDPGNGVWSSPAPRCLESLVAPACPP 1851

Query: 100 PDPVNGMA--AAVTKDIQFGSQIKYSCPGRYRLIGSSSANCIIISGNTVIMDKTTPVC 153
P NG HV + G I Y+C GY L+G C G IW C

Sbjct: 1852 PKIQNGHYIGGWSLYLP-GMTISTYCDPYLLVGRKQFIPTDGG--IWSOLDHYC 1904

Score = 36.7 bits (83), Expect = 0.12
Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PNLITDDP-----EPPIGYLANTECRPGYSGRPF-----STICLN--SWTSAK 88
P P D P F G+ + Y+C G G SI C W+S
Sbjct: 1523 PTLNSNDPYSNMKTSHNGTAVTYTCHGPDGQDLBELWGERSTICTSDPGVWSSSP 1582

Query: 89 DKCKRSCNPPDPVNGMAHVKDIQFGSQ--IKYSCPGRYRLIGSSSANCIIISGNTVY 145
+C + P+ N + V + P S I++ C G+ ++G+ C +G
Sbjct: 1583 PRCTSNCTAPFVEMAL-RVPGNRSPFSLTEILIRRCQPGFVWGSHTVQCQNGR--- 1638

Query: 146 WDKTTPVC 153
W K P C
Sbjct: 1639 WGEKLPIC 1646

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFPAPFNLTDDPPIGYLANTECRPGYS-GRPSII-----CLK--NSV 83
C P +P R P + PP G +NY C P G P +I C N V
Sbjct: 421 CPSPVPIPNGRHNGKPLEV-PPFGKAVNYTCDPHDRGTSFDLIGESTRICTSDPGNGV 479

Query: 84 WTSAKDKCR-RKSCNPPDPVNGMAHVK--IKDIQFGSQIKYSCPGRYRLIGSSSANCII 139
W+S +C C+ P + D G+ +X C Y S NC+
Sbjct: 480 WSPAPRCGILGHCOAPDHPFLAKLTQTNASDPPIGTSIAKTECRPEY-YGRPSITCL- 537

Query: 140 SGNTVIMDKTTPVC 153
++W+ +V
Sbjct: 538 --DNLWSSPPDYVC 549

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFPAPFNLTDDPPIGYLANTECRPGYS-GRPSII-----CLK--NSV 83
C P +P R P + PP G +NY C P G P +I C N V
Sbjct: 871 CPSPVPIPNGRHNGKPLEV-PPFGKAVNYTCDPHDRGTSFDLIGESTRICTSDPGNGV 929

Query: 84 WTSAKDKCR-RKSCNPPDPVNGMAHVK--IKDIQFGSQIKYSCPGRYRLIGSSSANCII 139
W+S +C C+ P + D G+ +X C Y S TC+
Sbjct: 930 WSPAPRCGILGHCOAPDHPFLAKLTQTNASDPPIGTSIAKTECRPEY-YGRPSITCL- 987

Query: 140 SGNTVIMDKTTPVC 153
++W+ +V
Sbjct: 988 --DNLWSSPPDYVC 999

>GSEQ:AAK41010 Human polypeptide SEQ ID NO 5941.
Length = 2044

Score = 256 bits (647), Expect = 8e-68
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLIALALVLLISFS-DCNVPEMLPFPAPFNLTDDPPIGYLANTECRPGYSGRPSII 76
G LLA +VLL + QCN PEMLPFPAPFNLTDDPPIGYLANTECRPGYSGRPSII
Sbjct: 30 GSLLAVVLLALVAMGQCNAPFEMLPFPAPFNLTDDPPIGYLANTECRPGYSGRPSII 89

Query: 77 ICLKNSWTSAKDKCRKSCNPPDPVNGMAHVKDIQFGSQIKYSCPGRYRLIGSSSANCII 136
ICLKNSWTS AKD+C+RSCNPPDPVNGM HVK IQFGSQIKYSC KGYRLIGSSSANCII
Sbjct: 90 ICLKNSWTS AKDKCRKSCNPPDPVNGMAHVKDIQFGSQIKYSCPGRYRLIGSSSANCII 149

Sbjct: 1933 YHGGVYTLKCEBDGYTLGSSPMSCQADNR---MDPELACTSRTHDLI 1979

Score = 43.8 bits (101), Expect = 9e-04

Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTYLYNECRPGY---SGRPSTICLNSVWTSADKCKRSCNPPDPVNG--MAHVI 111

Sbjct: 129 GSOIKYSCYGLIGSSATCIIISDVTWMDNETPICRIPCGLPPTIANGDFTS 188

Query: 112 DIOGSOIKYSCYGLIGSSATCIIISGNTV--IMDKRTPVC 153

Sbjct: 189 NFHGSVYTRCNMGSGGRKVFELVGEPSICTSNDQVIGMSPAQC 237

Score = 43.0 bits (99), Expect = 0.002

Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGYLYNECRPGY---GRPSITICLNSV--WTSADKCKRSCNPPDPVNG--MA 107

Sbjct: 575 DIOGSRINYSCTTGRLIGHSSAECILSNAHASTKPPICRIPCGLPPTIANGDFTS 634

Query: 108 HVIKDIOGSOIKYSCYGLIGSSATCIIISGNTV--IMDKRTPVC 153

Sbjct: 635 TNENHGVSVYTRCNMGSGGRKVFELVGEPSICTSNDQVIGMSPAQC 687

Score = 43.0 bits (99), Expect = 0.002

Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGTLYNECRPGY---SGRPSTICLNSVWTSADKCKRSCNPPDPVNG--MAHVI 110

Sbjct: 1283 LGAKSVYCDGGRKLGSSVSHCVLWGRSLMNSVPCETICRPFALLNGHTPS 1342

Query: 111 KDIOGSOIKYSCYGLIGSSATCIIISGNTV--IMDKRTPVC 158

Sbjct: 1343 GDIPGRKISYTCDDPHDRGMTFNLIGESTIRCTSDPHGNGV--WSSPAKCELSVA 1397

Score = 42.6 bits (98), Expect = 0.002

Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGYLYNECRPGYSGRPP---ITCLNSVWTSADKCKRSCNPPDPVNG--MA 107

Sbjct: 1025 DIOGSRINYSCTTGRLIGHSSAECILSNGTAMSTPPICRIPCGLPPTIANGDFTS 1084

Query: 108 HVIKDIOGSOIKYSCYGLIGSSATCIIISGNTV--IMDKRTPVC 153

Sbjct: 1085 TNENHGVSVYTRCNMGSGGRKVFELVGEPSICTSNDQVIGMSPAQC 1137

Score = 42.6 bits (98), Expect = 0.002

Identities = 31/112 (27%), Positives = 53/112 (46%), Gaps = 15/112 (13%)

Query: 57 IGTLYNECRPGY---SGRPPS---ITCLNSVWTSADKCKRSCNPPDPVNG--MAHVI 110

Sbjct: 1736 LGAKSVYCDGGRKLGSSVSHCVLWGRSLMNSVPCETICRPFALLNGHTPS 1795

Query: 111 KDIOGSOIKYSCYGLIGSSATCIIISGNTV--IMDKRTPVC 154

Sbjct: 1796 GDIPGRKISYTCDDPHDRGMTFNLIGESTIRCTSDPHGNGV--WSSPAKCE 1846

Score = 41.4 bits (95), Expect = 0.005

Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTLYNECRPGY---SGRPSTICLNSVWTSADKCKRSCNPPDPVNGMAHVIKD 112

Sbjct: 383 LGAKVYCDGGRKLGSSVSHCVLWGRSLMNSVPCETICRPFALLNGHTPS 441

Query: 113 IQ---RGSQIKYSCYGLIGSSATCIIISGNTV--IMDKRTPVC 153

Sbjct: 442 LEVFPGRKAVNYTCDDPHDRGMTFNLIGESTIRCTSDPHGNGV--WSSPAKCE 492

Score = 41.4 bits (95), Expect = 0.005

Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTLYNECRPGY---SGRPSTICLNSVWTSADKCKRSCNPPDPVNGMAHVIKD 112

Sbjct: 833 LGAKVYCDGGRKLGSSVSHCVLWGRSLMNSVPCETICRPFALLNGHTPS 891

Query: 113 IQ---RGSQIKYSCYGLIGSSATCIIISGNTV--IMDKRTPVC 153

Sbjct: 892 LEVFPGRKAVNYTCDDPHDRGMTFNLIGESTIRCTSDPHGNGV--WSSPAKCE 942

Score = 38.7 bits (88), Expect = 0.030

Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPIGYLYNECRPGY---GRPSITICLNSV--WTSADKCKRSCNPPDPVNG--MA 107

Sbjct: 1797 DIOGSRINYSCTTGRLIGHSSAECILSNAHASTKPPICRIPCGLPPTIANGDFTS 1856

Query: 100 PDPVNGM---AHVIRKDIOGSOIKYSCYGLIGSSATCIIISGNTV--IMDKRTPVC 153

Sbjct: 1857 PKIQNHVIGRHSVLYLP--GMTISTYCDRGVLYVGRIFCTDGG---IMSDQHNIC 1909

Score = 37.5 bits (85), Expect = 0.067

Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEWLPAPRPNLTDLP-----EPIGYLYNECRPGYSGRPP-----STICLKN-- 81

Sbjct: 619 IPCGLP---FTIANGDPISTNENHGVSVYTRCNMGSGGRKVFELVGEPSICTSND 675

Query: 82 --SVWTSADKCKRSCNPPDPVNGMAHVIKD---IQGSOIKYSCYGLIGSSA 135

Sbjct: 676 QVGWISGAPQCIIPNKCPTPVNENG--LVEDNNSLFLSLNVEVFPKQGPVMEGRPV 733

Query: 136 NCIIISGNTVIMDKRTPVC 153

Sbjct: 734 KQALNKF---WEPELDFSC 748

Score = 37.5 bits (85), Expect = 0.067

Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEWLPAPRPNLTDLP-----EPIGYLYNECRPGYSGRPP-----STICLKN-- 81

Sbjct: 169 IPCGLP---FTIANGDPISTNENHGVSVYTRCNMGSGGRKVFELVGEPSICTSND 225

Query: 82 --SVWTSADKCKRSCNPPDPVNGMAHVIKD---IQGSOIKYSCYGLIGSSA 135

Sbjct: 226 QVGWISGAPQCIIPNKCPTPVNENG--LVEDNNSLFLSLNVEVFPKQGPVMEGRPV 283

Query: 136 NCIIISGNTVIMDKRTPVC 153

Sbjct: 284 KQALNKF---WEPELDFSC 298

Score = 36.7 bits (83), Expect = 0.12
Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PNTLTDPE-----EPPIGYLANVECRPGYSGRP-----SIICLKN-----SWTSAX 88
P N DF F G + Y+C G G SI C VM+S
Sbjct: 1528 PTISNDGYSNRNSFHNHGVTVYQCHNGDGEQLFELVGENSIYCSKDYGVWSSSP 1587
Query: 89 DCKRRCANPPDPVNGMAHVIKIDIOFSGQIKYSCPKGYRLIGSSSANTCI 145
+C + P+ N + V + F S I++C G++G+ C +G
Sbjct: 1588 PRCISTNKKCAEVEYENAI-RVGNRNSFSLIHLIFRCQGFVNGSHVQCQNR---- 1643
Query: 146 WDKTPVC 153
W K P C
Sbjct: 1644 WQKPLPHC 1651

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPNLTDDPEPIGYLANVECRPGYS-GRPFSII-----CLK-----NSV 83
C P +P R T + PP G +NY C P G F +I C N V
Sbjct: 426 CPEPVIYNGRHNGKPLEV-FPPGKAVNYTCDHPDRGTSFDLIGSTRCTSDQNGNV 484
Query: 84 WMSADKCK-RKSCNPPDPVNGMAHVIKIDIOFSGQIKYSCPKGYRLIGSSSANTCI 139
W+S +C C+ P + D C+ +RY C Y S TC+
Sbjct: 485 WSSPAPRCGLGHCOAHDFLPAKLKTYMAADPPIGTSIKYECRPEY-YGRPFSITCL- 542
Query: 140 SGNVTYIMDKTPVC 153
+ +W + VC
Sbjct: 543 --DNLWSSPRDVC 554

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPNLTDDPEPIGYLANVECRPGYS-GRPFSII-----CLK-----NSV 83
C P +P R T + PP G +NY C P G F +I C N V
Sbjct: 876 CPEPVIYNGRHNGKPLEV-FPPGKAVNYTCDHPDRGTSFDLIGSTRCTSDQNGNV 934
Query: 84 WMSADKCK-RKSCNPPDPVNGMAHVIKIDIOFSGQIKYSCPKGYRLIGSSSANTCI 139
W+S +C C+ P + D C+ +RY C Y S TC+
Sbjct: 935 WSSPAPRCGLGHCOAHDFLPAKLKTYMAADPPIGTSIKYECRPEY-YGRPFSITCL- 992
Query: 140 SGNVTYIMDKTPVC 153
+ +W + VC
Sbjct: 993 --DNLWSSPRDVC 1004

>GSEQ:AM39224 Human polypeptide SEQ ID NO 2369.

Length = 2044

Score = 256 bits (647), Expect = 8e-68
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLALVALLSSFS-DQCNVPEMLPFARPNLTDDPEPIGYLANVECRPGYSGRPSI 76
G LLA AYL + QCN PMLEPAPRNLTDDPEPIGYLANVECRPGYSGRPSI
Sbjct: 30 GSLAVVLLALFVANGCNAPEMLPFARPNLTDDPEPIGYLANVECRPGYSGRPSI 89
Query: 77 ICLNSWTSADKCKRRCNPPDPVNGMAHVIKIDIOFSGQIKYSCPKGYRLIGSSSANT 136
ICLNKSWT AKD+C+RKSCNPPDPVNG HVIK IOPGQIKYSC KGYRLIGSSSANT
Sbjct: 90 ICLNSWTSADKCKRRCNPPDPVNGMAHVIKIDIOFSGQIKYSCPKGYRLIGSSSANT 149
Query: 137 CIISGNTVIMDKTPVC 154
CIISG+TVIMDN+TP+CD

Sbjct: 150 CIISGNTVIMDKTPVC 167

Score = 176 bits (442), Expect = 9e-44
Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LSSFDQCNVPEMLPFARPNLTDDPEPIGYLANVECRPGYSGRPSIICLNKSWTSAXDKCKR 87
LS + C PE PFA PM +DPEP+QT IYECRPGY G+ PSI CL+N VM+S
Sbjct: 1394 LSVRAGCKTPQGFPAFPASPPIINDPEPIGYLANVECRPGYSGMFTISCLNEMWSSV 1453
Query: 88 KRCRCRRCNPPDPVNGMAHVIKIDIOFSGQIKYSCPKGYRLIGSSSANTCIISGNTVIM 147
+D C+RKSC PP+P NCM H+ D OFGS + YSC +GRILIG S TC+SGN V MD
Sbjct: 1454 EDNCRKRCGPEPFGNGVHNTDIOFSGVTSVNSCNGRILIGSFTVLVSQNVYMD 1513
Query: 148 NRTVPCD 154
K P+C+
Sbjct: 1514 KRAPICE 1520

Score = 166 bits (417), Expect = 8e-41
Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 35 CNVPEMLPFARPNLTDDPEPIGYLANVECRPGYSGRPSIICLNKSWTSAXDKCKR 94
C P+ FA+ T+ +PPIGT L YECRP Y GRPSI CL N VM+S KD CKR
Sbjct: 948 COAPDHFLPAKLKTYMAADPPIGTSIKYECRPEYGRPFSITCLDNLWSSPRDVCCKR 1007
Query: 95 SCNPPDPVNGMAHVIKIDIOFSGQIKYSCPKGYRLIGSSSANTCIISGNTVIMDKTPVC 153
SC+ PDPVNGM HVI DIO GS+I YSC +GRILIG SSA CI+SGNT W K P+C
Sbjct: 1008 SCRTPPDPVNGMAHVIKIDIOGSRINYSCTGHRILIGSSABECILSGNTAMWSTKPPIC 1066

Score = 164 bits (412), Expect = 3e-40
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNVPEMLPFARPNLTDDPEPIGYLANVECRPGYSGRPSIICLNKSWTSAXDKCKR 94
C P+ FA+ T+ +PPIGT L YECRP Y GRPSI CL N VM+S KD CKR
Sbjct: 498 COAPDHFLPAKLKTYMAADPPIGTSIKYECRPEYGRPFSITCLDNLWSSPRDVCCKR 557
Query: 95 SCNPPDPVNGMAHVIKIDIOFSGQIKYSCPKGYRLIGSSSANTCIISGNTVIMDKTPVC 153
SC+ PDPVNGM HVI DIO GS+I YSC +GRILIG SSA CI+SGNT W K P+C
Sbjct: 558 SCRTPPDPVNGMAHVIKIDIOGSRINYSCTGHRILIGSSABECILSGNTAMWSTKPPIC 616

Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFDQCNVPEMLPFARPNLTDDPEPIGYLANVECRPGYSGR-PSIICLNKSWTS 86
L S S C P + A T D P G + Y C PGY R S+ C W+
Sbjct: 745 LPSCSNVQPPDPVLAARTORDKD-NFSPQGEVYSCPEPYDLRGAASNRCTPOGDWSP 803
Query: 87 AKDCKRRCN-PPDPVNGMAHVIKIDIOFSGQIKYSCPKGYRLIGSSSANTCIISGNTV 145
A C+ KSC +NG ++O G+++ + C +O++L GSS++ C++G +
Sbjct: 804 AALTCBVSQCDPMQGLNGRVLPVNIQLAKAVDVDEDFOLKSSASVCVLAAMEL 863
Query: 146 WDKTPVC 154
W++ PNC+
Sbjct: 864 WNSVPC 872

Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFDQCNVPEMLPFARPNLTDDPEPIGYLANVECRPGYSGR-PSIICLNKSWTS 86
L S S C P + A T D P G + Y C PGY R S+ C W+
Sbjct: 295 LPSCSNVQPPDPVLAARTORDKD-NFSPQGEVYSCPEPYDLRGAASNRCTPOGDWSP 353

Query: 87 AKDKCRKRCN--PDPVNGAHVINDIOFSGQIKYSCPGYRLIGSSSANCIIISGNTV 145
A C+ KSC + +NG + +Q G+++ + C +G+L GSS++ C++G +
Sbjct: 354 AATPCVSCDPPFQGLANGVLE PVTLDQAKVDFVCDGFLQGLGSSASVLAGESL 413

Query: 146 WDKRTPVCD 154
W++ PVC+
Sbjct: 414 WNSVPCVE 422

Score = 64.8 bits (155), Expect = 4e-10
Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)

Query: 28 LSSFDQCNVEMLPFAPFNTLDDPFPITGLATECRPGYSR--PFSIIICLNKSNVWTS 86
L S S C P + + D F G + Y C PGY R S+ C W+
Sbjct: 1195 LPSGRVCOPEPILHGEHPHSHQD--NFPQGEVYSCPGYDLRGAASLHCTPQGMSP 1233

Query: 87 AKDKCRKRCNPPDPV--NGAHVINDIOFSGQIKYSCPGYRLIGSSSANCIIISGNTV 145
+C KSC + +G + +Q G+++ + C +G+L GSS + C++ G +
Sbjct: 1254 EAPRCAYKSCDPLGLPHGRVLFPLNQLAKVSVCDGFLKGSVSHCVLWGRSL 1313

Query: 146 WDKRTPVCD 154
W+N PVC+
Sbjct: 1314 WNSVPCVE 1322

Score = 61.3 bits (146), Expect = 5e-09
Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)

Query: 49 LDDPFPITGLATECRPGYSR--PFSIIICLNKSNVWTSADKCRKRCNPPDPV--NGM 106
L+ F G + Y C P Y R S+ C W+ +C KSC + +G
Sbjct: 1668 LSHQDNFSPQGEVYSCPGYDLRGAASLHCTPQGMSPRATVKSDDPLQGLPHR 1727

Query: 107 AHVINDIOFSGQIKYSCPGYRLIGSSSANCIIISGNTVINDKRTVPC 154
+ + +Q G+++ + C +G+L G S++ C++G +W++ PVC+
Sbjct: 1728 VLLPLNQLAKVSVCDGFLKGSASVLAGKALMNSVPCVE 1775

Score = 48.0 bits (112), Expect = 5e-05
Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)

Query: 26 LLLSFDQCNV--PMLPFPAPFNTLDDPFPITGLATECRPGYS--GRPFSIICL 79
L+ SS D C P PF ++ D +F G+ +NY C G+ G P S CL
Sbjct: 1448 LVMSSVDNCRKRCSCGPPFPNGMHIINDYQF--GTVVYSCNGRFLIGSP-STYCL 1504

Query: 80 ---KSNVWTSADKCRKRCNPPDPVNGAHVINDIOF--GSOIKYSCRG-----YR 128
N W C+ SC PF NG + F G+ + Y C G +
Sbjct: 1505 VSGNNVWMDKAPICELIISCEPPTISNGDYSNNRTSFHNGTVVYQCHGPDGQLE 1564

Query: 129 LIGSSSANCIIISGNTV--INDKRTVPCDSELK 158
L+G S C + V +W + P C S K
Sbjct: 1565 LVGRSIYCTSKDQVGMSSPPRCISTNK 1595

Score = 46.5 bits (108), Expect = 1e-04
Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)

Query: 57 IGTLYATECRPGY--SGRPFSS--IICLNKSNVWTSADKCRKRCNPPDPVNG--MAHYI 110
+G +++ C G+ GR S ++ +W S+ C++ C NPP +NG
Sbjct: 1736 LQAKVSVCDGFLKGSASVLAGKALMNSVPCVEIFCPVPALINGHRTGTF 1795

Query: 111 KDIOFSGQIKYSCP-----KGYRLIGSSSANCII--GNTVINDKRTVPCD 154
DI +G +I Y+C + LIG SS C GN V W + P C +
Sbjct: 1796 GIPIYGREISVACDHPDRGATFNILIGSSIRCTSPDQGNV--WSPAPRCE 1846

Score = 43.8 bits (101), Expect = 9e-04
Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)

Query: 58 GTYLATECRPGY--GRPFSIICLNKSNVWTSADKCRKRCNPPDPVNGAHV--RD 112
G + +Y C PGY G+ F I C +W+ CK +C P +NG++ + R
Sbjct: 1875 GMTISYCDPGYLVAGKF--IFCTDQIGMSQLDHCKVCNCSPELF--MNGISKELEKRV 1932

Query: 113 IOFSGQIKYSCPGYRLIGSSSANCIIISGNTVINDKRTVPCDSELK 162
+G + C GY L GS + C MD C S A +
Sbjct: 1933 YHGGVYTLKCEDGYTLGSSPMSCQADNR--WDPLAKTSRAIDALI 1979

Score = 43.8 bits (101), Expect = 9e-04
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTYLATECRPGY--SGRPFSS--IICLNKSNVWTSADKCRKRCNPPDPVNG--MAHYI 111
G+ + Y C GY S II +W+ C R C P NG ++ +
Sbjct: 129 GSOIKYSCPGYRLIGSSSANCIIISGNTVINDKRTVPCDSELK 188

Query: 112 KDIOFSGQIKYSCP-----YRLIGSSSANCIIISGNTV--INDKRTVPC 153
+ +GS + Y C G + L+G S C + + V IW P C C
Sbjct: 189 NPHYSVVTTCNPSGGRKVFELVGSFYTCTSDNDQVIGSGPAQC 237

Score = 43.0 bits (99), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPPIGTLYATECRPGY--GRPFSIICLNKSNV--WTSADKCRKRCNPPDPVNG--MA 107
+ +G+ +NY C G+ G + L + W++ C+R C P NG ++
Sbjct: 575 DIVQSRINTSCGTHRLIHGSAECIISGNAAHMSRPLIOGIPGAPLINDGPFIS 634

Query: 108 HVIKDIOFSGQIKYSCP-----YRLIGSSSANCIIISGNTV--INDKRTVPC 153
+ + +GS + Y C G + L+G S C + + V IW P C
Sbjct: 635 TMRNPHYSVVTTCNPSGGRKVFELVGSFYTCTSDNDQVIGSGPAQC 687

Score = 43.0 bits (99), Expect = 0.002
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGTLYATECRPGY--SGRPFSS--IICLNKSNVWTSADKCRKRCNPPDPVNG--MAHYI 110
+G +++ C G+ S ++ S+W ++ C+ C NPP +NG
Sbjct: 1283 LQAKVSVCDGFLKGSASVSHCVLWGRBLMNSVPCVEHICPVPALINGHRTGTS 1342

Query: 111 KDIOFSGQIKYSCP-----KGYRLIGSSSANCIIIS--GNTVINDKRTVPCDSELK 158
DI +G +I Y+C + LIG S+ C GN V W + P C + +
Sbjct: 1343 GDIPYGREISVACDHPDRGATFNILIGESTIRCTSDPHGNGV--WSPAPRCELSVR 1397

Score = 42.6 bits (98), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPPIGTLYATECRPGYSGRPFSS--IICLNKSNVWTSADKCRKRCNPPDPVNG--MA 107
+ +G+ +NY C G+ S ++ S+W ++ C+ C NPP +NG
Sbjct: 1025 DIQVSRINTSCGTHRLIHGSAECIISGNTVWTSAPRICRIGPPTLINDGPFIS 1084

Query: 108 HVIKDIOFSGQIKYSCP-----YRLIGSSSANCIIISGNTV--INDKRTVPC 153
++ +GS + Y C G + L+G S C + + V IW P C
Sbjct: 1085 TMRNPHYSVVTTCNIGSRKVFELVGSFYTCTSDNDQVIGSGPAQC 1137

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTLYATECRPGY--SGRPFSS--IICLNKSNVWTSADKCRKRCNPPDPVNGAHVIND 112

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTALNTECRPGY-----SGRPSITCLKNSWTSADKCKRKNPPDPVNGAHVTKD 112
+G +++ C G+ S ++ S+W S+ C++ C +P NG H K
+G +++ C G+ S ++ S+W S+ C++ C +P NG H K
Sbjct: 833 LGAIVDFVCEGOLKGSASVCYLWGESLMSNVCEIFCPSPVPIWG-RHTGKP 891

Query: 113 IQ---FSGQIKYSCF-----KGYRLIGSSANCI--SGNTVIMDKKTPVC 153
++ FG + Y+C S + LG S+ C GN V W + P C
Sbjct: 442 LEVFPFGKTVNYTCDBPHDRGTSFDLIGESTRICTSDPQNGV-WSSPAPRC 492

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFARPTNLTDPF-----EPPIGYLNTYECRPGYSGRPF-----SIICLN-- 81
+P LP PT DF P G+ + Y C PG GR SI C N
Sbjct: 619 IFCGLP---PTINGDFISTNRENFHYSGVTVTRCNPSGGRKVFELVGEPSITCTSDND 675

Query: 82 --SWTSADKCKRCKRKNPPDPVNGAHVTKD---IQFSGQIKYSCFGRYRLIGSSA 135
+W+ +C + PP+ NG+ ++ D +++ C G+ + G
Sbjct: 676 QVQVSGAPQCIIIPKCTPPNVNGI--LVSDNRSLFELNEVVEPQCQPGVAKGRNV 733

Query: 136 TCIIISGNTVIMDKKTPVC 153
C W+ + P C
Sbjct: 734 KCOALNR---WEPELPSC 748

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFARPTNLTDPF-----EPPIGYLNTYECRPGYSGRPF-----SIICLN-- 81
+P LP PT DF P G+ + Y C PG GR SI C N
Sbjct: 169 IFCGLP---PTINGDFISTNRENFHYSGVTVTRCNPSGGRKVFELVGEPSITCTSDND 225

Query: 82 --SWTSADKCKRCKRKNPPDPVNGAHVTKD---IQFSGQIKYSCFGRYRLIGSSA 135
+W+ +C + PP+ NG+ ++ D +++ C G+ + G
Sbjct: 226 QVQVSGAPQCIIIPKCTPPNVNGI--LVSDNRSLFELNEVVEPQCQPGVAKGRNV 283

Query: 136 TCIIISGNTVIMDKKTPVC 153
C W+ + P C
Sbjct: 284 KCOALNR---WEPELPSC 298

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPPIGTVLNTYECRPGYS-GRPSII-----CLK-----NSVTSADKCKRCKRKNPPDPVNGAHVTKD 99
+ P G +Y C G F+I C N W+S +C+ +C +P
Sbjct: 179 DTPYGRKISVACDHPHRCMTNLTNGESIRCTSDPQNGVMSAPRACELSPACRHP 1856

Query: 100 EDPVNG--AHYIKDIQFSGQIKYSCFGRYRLIGSSANCIISGNTVIMDKKTPVC 153
P NG HV + G I Y+C GY L+G C G IW C
Sbjct: 1857 PRIONGHYIGHVLPLP-GMTISVTCDPGLVVGKGFICTDQ--IWSOLDHYC 1909

Score = 36.7 bits (83), Expect = 0.12

Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PTNLTDPF-----EPPIGYLNTYECRPGYSGRPF-----SIICLN-----SVWTSAR 88
PT DF F GT + Y+C G G SI C W+S
Sbjct: 1528 PTISNDDEFYSNNRSTFPHNGTVVYCHTQDQDQFELVGEISITCTSDQVGVMSPP 1587

Query: 89 DCKRCKRKNPPDPVNGAHVTKDIOFSGO---IKYSCFGRYRLIGSSANCIISGNTVIMDKKTPVC 145
+C + P+ N + V + P S I++ C G+ ++G + C +G
Sbjct: 1588 PRCTISNCTAPTEVNAI-RVGNRSTFLTRIRFCQGRVWMSHTVQCTNGR--- 1643

Query: 146 WDKKTPVC 153
W K P C
Sbjct: 1644 WGRPLPFC 1651

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPTNLTDPEPIGYLNTYECRPGYS-GRPSII-----CLK-----NSV 83
C P +P R T + PP G +NY C P G F+I C N V
Sbjct: 426 CESPVIIPNGRHTGKPLEV-FPPGKAVNYTCDBPHDRGTSFDLIGESTRICTSDPQNGV 484

Query: 84 WTSADKCKRCKRKNPPDPVNGAHV---IKDIQFSGQIKYSCFGRYRLIGSSANCI 139
W+S +C C+ P + D G+ +XY C Y S TC+
Sbjct: 485 WSSPAPRCIGLHCQADPHFLAKIKQTNA SDPFGISLKYECREY-YGRPSITCL- 542

Query: 140 SGNTVIMDKKTPVC 153
+ ++W + VC
Sbjct: 543 --DNLVWSSPFDVC 554

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPTNLTDPEPIGYLNTYECRPGYS-GRPSII-----CLK-----NSV 83
C P +P R T + PP G +NY C P G F+I C N V
Sbjct: 876 CESPVIIPNGRHTGKPLEV-FPPGKAVNYTCDBPHDRGTSFDLIGESTRICTSDPQNGV 934

Query: 84 WTSADKCKRCKRKNPPDPVNGAHV---IKDIQFSGQIKYSCFGRYRLIGSSANCI 139
W+S +C C+ P + D G+ +XY C Y S TC+
Sbjct: 935 WSSPAPRCIGLHCQADPHFLAKIKQTNA SDPFGISLKYECREY-YGRPSITCL- 992

Query: 140 SGNTVIMDKKTPVC 153
+ ++W + VC
Sbjct: 993 --DNLVWSSPFDVC 1004

>GSEQ:ABH11782 Human CRI protein homologue, SBO ID NO:2152.
Length = 2044

Score = 256 bits (647), Expect = 8e-68
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLAALVLLLSFS-DQCNVPEMLPFARPTNLTDPEPIGYLNTYECRPGYSGRPSI 76
G LLA +VLL + QCN PEMLPFARPTNLTDPEPIGYLNTYECRPGYSGRPSI
Sbjct: 30 GSLLAVVLLALPVAMQCNAPPEMLPFARPTNLTDPEPIGYLNTYECRPGYSGRPSI 89

Query: 77 ICLKNSWTSADKCKRCKRKNPPDPVNGAHVTKDIOFSGQIKYSCFGRYRLIGSSANCI 136
ICLKNSWTSADKCKRCKRKNPPDPVNGAHVTKDIOFSGQIKYSCFGRYRLIGSSANCI
Sbjct: 90 ICLKNSWTSADKCKRCKRKNPPDPVNGAHVTKDIOFSGQIKYSCFGRYRLIGSSANCI 149

Query: 137 CIIISGNTVIMDKKTPVC 154
CIIISGNTVIMDKKTPVC
Sbjct: 150 CIIISGNTVIMDKKTPVC 167

<http://patients.incyte.com/8000/csi-bio/SeeServer/SeeServer>

5/5/03 8:58 PM

5/5/03 8:58 PM

Identifiers = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTLVNTECRPGY----SGRPSTICLKNVWTSADKCKRKRSCNPPDPVNG--MAHVI 111
+G + Y C GY S II +W + C R C RP NG ++ +
Sbjct: 129 GSOIKYSCGTHLIGSSATCISDGVWINDETPICRIRICGLPTIINDGPTIS 188

Query: 112 DIQFSGQIKYSCFPG-----YRLIGSSATCIIISGNTV--IWDNKTTPVC 153
++ +G S + Y C G +L+G S C + + V IW P C
Sbjct: 189 NRENFHYSVTVYRCNPGSGRKYFELVGEPSIYCTSDNDQVIGSGAPQC 237

Score = 43.0 bits (99), Expect = 0.002
Identifiers = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTYLATECRPGY--GRPSITICLKNV--WTSADKCKRKRSCNPPDPVNG--MA 107
+ +G + NY C G+ G + L + W++ C+R C RP NG ++
Sbjct: 575 DIQVSRINSCYTHRLIGHSSABECILSGNAHMTKRPICRIRICGLPTIINDGPTIS 634

Query: 108 HVIKDIOFSGQIKYSCFPG-----YRLIGSSATCIIISGNTV--IWDNKTTPVC 153
++ +G S + Y C G +L+G S C + + V IW P C
Sbjct: 635 TNRNHFHYSVTVYRCNPGSGRKYFELVGEPSIYCTSDNDQVIGSGAPQC 687

Score = 43.0 bits (99), Expect = 0.002
Identifiers = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGTIVNTECRPGY----SGRPSTICLKNVWTSADKCKRKRSCNPPDPVNG--MAHVI 110
+G + + + C G+ S ++ S+W ++ C+ C NRP +NG
Sbjct: 1283 LGANVSVCDDECFRLKGSVSHCVLWGRSLMNSVPCCHITFCIPALINHGHTPS 1342

Query: 111 KDIOFSGQIKYSCFPG-----KGYRLIGSSATCIIISGNTV--IWDNKTTPVC 158
DI +G + I Y+C +LIG S+ C GN V W + P C ++
Sbjct: 1343 GDIPEKREISYCTDPHDPDGMFNLIGESTIRCTSDPHNGV--WSSPAPRCELSTVA 1397

Score = 42.6 bits (98), Expect = 0.002
Identifiers = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTYLATECRPGYSGRPF--ITCLKNVWTSADKCKRKRSCNPPDPVNG--MA 107
+G + + + C G+ S ++ S+W ++ C+R C RP NG ++
Sbjct: 1023 DIQVSRINSCYTHRLIGHSSABECILSGNTAHMTKRPICRIRICGLPTIINDGPTIS 1084

Query: 108 HVIKDIOFSGQIKYSCFPG-----YRLIGSSATCIIISGNTV--IWDNKTTPVC 153
++ +G S + Y C G +L+G S C + + V IW P C
Sbjct: 1085 TNRNHFHYSVTVYRCNPGSGRKYFELVGEPSIYCTSDNDQVIGSGAPQC 1137

Score = 42.6 bits (98), Expect = 0.002
Identifiers = 53/112 (46%), Gaps = 15/112 (13%)

Query: 57 IGTIVNTECRPGY--SGRPF--ITCLKNVWTSADKCKRKRSCNPPDPVNG--MAHVI 110
+G + + + C G+ GR S ++ +W S+ C++ C NRP +NG
Sbjct: 1736 LGANVSVCDDECFRLKGRSAHSVCVLAQKALMNSVPCDEQICCPALINHGHTPS 1795

Query: 111 KDIOFSGQIKYSCFPG-----KGYRLIGSS--ATCIIISGNTV--IWDNKTTPVC 154
DI +G ++ Y+C +LIG S+ T GN V W + P C
Sbjct: 1796 GDIPEKREISYCTDPHDPDGMFNLIGESTIRCTSDPHNGV--WSSPAPRCELSTVA 1846

Score = 41.4 bits (95), Expect = 0.005
Identifiers = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTIVNTECRPGY--SGRPFSTICLKNVWTSADKCKRKRSCNPPDPVNGMAHVIKD 112
+G + + + C G+ S ++ S+W S+ C++ C +PP NG H K
Sbjct: 383 LGAKVDFVCDGFLKGSASGYCVLAGESIMNSVPCVCEQICPSPVPIVNG--RHTGRK 441

Query: 113 IQ---FSGQIKYSCP-----KGYRLIGSSATCII--SGNTVIMDNKTTPVC 153
++ FG + Y+C +LIG S+ C GN V W + P C
Sbjct: 442 LEVFPFKAVNTVCDPHDGRGTSFDLIGESTIRCTSDPHNGV--WSSPAPRCELSTVA 492

Score = 41.4 bits (95), Expect = 0.005
Identifiers = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTIVNTECRPGY----SGRPSTICLKNVWTSADKCKRKRSCNPPDPVNGMAHVIKD 112
+G + + + C G+ S ++ S+W S+ C++ C +PP NG H K
Sbjct: 833 LGAKVDFVCDGFLKGSASGYCVLAGESIMNSVPCVCEQICPSPVPIVNG--RHTGRK 891

Query: 113 IQ---FSGQIKYSCP-----KGYRLIGSSATCII--SGNTVIMDNKTTPVC 153
++ FG + Y+C +LIG S+ C GN V W + P C
Sbjct: 892 LEVFPFKAVNTVCDPHDGRGTSFDLIGESTIRCTSDPHNGV--WSSPAPRCELSTVA 942

Score = 38.7 bits (88), Expect = 0.030
Identifiers = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPIGTYLATECRPGY--GRPSITICLKNV--WTSADKCKRKRSCNPPDPVNG--MA 107
+ P G +Y C P G F++I N W+S +C+ +C +P
Sbjct: 1797 DIPEKREISYCTDPHDPDGMFNLIGESTIRCTSDPHNGV--WSSPAPRCELSTVA 1856

Query: 100 PDPVNGM--AHVTKDIOFSGQIKYSCFPGYRLIGSSATCIIISGNTVIMDNKTTPVC 153
P NG HV + G I Y+C GY L+G C G IW C
Sbjct: 1857 PRIONGHYIGHVSILYLP--GNTISYCTDPGVLYLWGRKFICTDQG--INSQLDHYC 1909

Score = 37.5 bits (85), Expect = 0.067
Identifiers = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPAPRPYTLTDPF-----EPIGTYLATECRPGYSGRPF-----STICLKN-- 81
+P LP PT DF P G+ + Y C PG GR SI C N
Sbjct: 619 IFCGLP--PTIANGDFISTNRNHFHYSVTVYRCNPGSGRKYFELVGEPSIYCTSDND 675

Query: 82 --SVWTSADKCKRKRSCNPPDPVNGMAHVIKD---IQFSGQIKYSCPKGYRLIGSSA 135
++ +C + PP+ NG+ ++ D ++ C G+ + G
Sbjct: 676 QVIGTSGAPQCIIINCKCTPPVNGI--LVSNDMSLPSLNEVEYERCPQPFVWKPGRV 733

Query: 136 TCIISGNTVIMDNKTTPVC 153
C W+ + P C
Sbjct: 734 KQALNR--WEPELPSC 748

Score = 37.5 bits (85), Expect = 0.067
Identifiers = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPAPRPYTLTDPF-----EPIGTYLATECRPGYSGRPF-----STICLKN-- 81
+P LP PT DF P G+ + Y C PG GR SI C N
Sbjct: 169 IFCGLP--PTIANGDFISTNRNHFHYSVTVYRCNPGSGRKYFELVGEPSIYCTSDND 225

Query: 82 --SVWTSADKCKRKRSCNPPDPVNGMAHVIKD---IQFSGQIKYSCPKGYRLIGSSA 135
++ +C + PP+ NG+ ++ D ++ C G+ + G
Sbjct: 226 QVIGTSGAPQCIIINCKCTPPVNGI--LVSNDMSLPSLNEVEYERCPQPFVWKPGRV 283

Query: 136 TCIISGNTVIMDNKTTPVC 153
C W+ + P C
Sbjct: 284 KQALNR--WEPELPSC 298

Score = 36.7 bits (83), Expect = 0.12
Identifiers = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PNLITDPP-----EPPIGTALNTECRPGYSGRPF-----SIITLKN-----SIWTSAX 88
PF DP F GP + Y+C G G SI C W+S
Sbjct: 1528 PHSNGPFSNNRSTFHHGTAVTYOCHNGDGBQLFELVGRSRTSYTSDQVSWSSFP 1587

Query: 89 DECKRSKSNPDVPMGMAHVIKDIOFGSQ---IKYSCPKGYRLIGSSSANCIIISGNTVI 145
+C + F+ N + V + F S I++ C G+ ++GS + C +G
Sbjct: 1588 PHSCTSTKTAPEYENAI-RVPGNSPFSILNEXIRFCQPGFVWGSHTVOCQNGR--- 1643

Query: 146 WDKTPVC 153
W R P C
Sbjct: 1644 WGRPLPHC 1651

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/114 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPAPARNLTDPEPIGTALNTECRPGYS-GRPSII-----CLK-----NSV 83
C P +P R T + FP G +NY C P G P +I C N V
Sbjct: 426 CPSPVPIENGHTGKPLEY-FPFGKAVNYTCDPHDGTSPDLIGESTIRCTSDPGNGV 484

Query: 84 WTSADCKK-RKSCNPPDPVNGMAHV---IKDIOFGSQIKYSCPKGYRLIGSSSANCII 139
W+S +C C+ P + D G+ +RY C Y S TC+
Sbjct: 485 WSSPAPRCGLGHQAEDHPLFAKLKTQTNASDPPIGTSIAKTECRPEY-YGRPSITCL- 542

Query: 140 SGNVTIMDKTPVC 153
+ ++W + VC
Sbjct: 543 --DNLWSSPMDVC 554

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/114 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPAPARNLTDPEPIGTALNTECRPGYS-GRPSII-----CLK-----NSV 83
C P +P R T + FP G +NY C P G P +I C N V
Sbjct: 876 CPSPVPIENGHTGKPLEY-FPFGKAVNYTCDPHDGTSPDLIGESTIRCTSDPGNGV 934

Query: 84 WTSADCKK-RKSCNPPDPVNGMAHV---IKDIOFGSQIKYSCPKGYRLIGSSSANCII 139
W+S +C C+ P + D G+ +RY C Y S TC+
Sbjct: 935 WSSPAPRCGLGHQAEDHPLFAKLKTQTNASDPPIGTSIAKTECRPEY-YGRPSITCL- 992

Query: 140 SGNVTIMDKTPVC 153
+ ++W + VC
Sbjct: 993 --DNLWSSPMDVC 1004

>GSEQ:ABG00287 Novel human diagnostic protein #278.

Length = 2039

Score = 256 bits (647), Expect = 8e-68
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLAALVLLSFS-DOCNPEMLPAPARNLTDPEPIGTALNTECRPGYSGRPSI 76
G LLA +YLL + OCN PEMLPAPARNLTDPEPIGTALNTECRPGYSGRPSI
Sbjct: 25 GSLLAVVLLALPVAMGQNAPEMLPAPARNLTDPEPIGTALNTECRPGYSGRPSI 84

Query: 77 ICLKNSWTSAXDKCKRSKSNPPDPVNGMAHVIKDIOFGSQIKYSCPKGYRLIGSSSANCII 136
ICLKNSWTF AKD+C-RKSCNPPDPVNGM HVIK IOFGSQIKYSC KGYRLIGSSSANCII
Sbjct: 85 ICLKNSWTSAXDKCKRSKSNPPDPVNGMAHVIKIOFGSQIKYSCPKGYRLIGSSSANCII 144

Query: 137 CIISGNTVIMDKTPVC 154
CIISG+TVIMDN+TP+CD
Sbjct: 145 CIISGNTVIMDKTPVC 162

Score = 176 bits (443), Expect = 9e-44

Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LSSFDQCNPEMLPAPARNLTDPEPIGTALNTECRPGYSGRPSIIICLKNSWTSAXDKCKR 87
LS + C PE FFA PT +DEFT+GT LNTERRPT G+ FSI CLN+ W+S
Sbjct: 1389 LSVRAHGTCTPFPFASPTIINDPEPVGSLNTECRPGYSGRPSIIICLKNSWTSAXDKCKR 1448

Query: 88 KDKCKRSKSNPPDPVNGMAHVIKDIOFGSQIKYSCPKGYRLIGSSSANCIIISGNTVI 147
+D C+RSC PP+P NGM H+ D OFGS + YSC +G+RLGS S TC++SGN V WD
Sbjct: 1449 EDNCRKSCGPEPEFGMAHVIINTDQFSGTWSVSCNCFRLIGSHPTCLVAGNNTWD 1508

Query: 148 NKTTPVC 154
K P+C+
Sbjct: 1509 KKAPICE 1515

Score = 166 bits (417), Expect = 8e-41
Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 35 CNVPEMLPAPARNLTDPEPIGTALNTECRPGYSGRPSIIICLKNSWTSAXDKCKR 94
C P+ FA+ T+ +FPITG L YECRP Y GRPSI CL N W+S KD CKR
Sbjct: 943 COADHPLFAKLKTQTNASDPPIGTSIAKTECRPEY-YGRPSITCLDNLWSSPMDVC 1002

Query: 95 SCNPPDPVNGMAHVIKDIOFGSQIKYSCPKGYRLIGSSSANCIIISGNTVIMDKTPVC 153
SC+ PDPVNGM HVI DIO GS+I YSC G+RLIG SSA CI+SGNT W K P+C
Sbjct: 1003 SCKTPDPVNGMAHVIKDIOVGSRLNTSCTGHRLLIGSSSANCIIISGNTVIMDKTPVC 1061

Score = 164 bits (412), Expect = 3e-40
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNVPEMLPAPARNLTDPEPIGTALNTECRPGYSGRPSIIICLKNSWTSAXDKCKR 94
C P+ FA+ T+ +FPITG L YECRP Y GRPSI CL N W+S KD CKR
Sbjct: 493 COADHPLFAKLKTQTNASDPPIGTSIAKTECRPEY-YGRPSITCLDNLWSSPMDVC 552

Query: 95 SCNPPDPVNGMAHVIKDIOFGSQIKYSCPKGYRLIGSSSANCIIISGNTVIMDKTPVC 153
SC+ PDPVNGM HVI DIO GS+I YSC G+RLIG SSA CI+SGNT W K P+C
Sbjct: 553 SCKTPDPVNGMAHVIKDIOVGSRLNTSCTGHRLLIGSSSANCIIISGNTVIMDKTPVC 611

Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFDQCNPEMLPAPARNLTDPEPIGTALNTECRPGYSGR-PSIIICLKNSWTSAXDKCKR 86
L S S C P + A T D P G +Y C PGT R S+ C W+
Sbjct: 740 LPSCSNVQPPDVLAERKTRD-RFSPQEVFISCEPGIDLRGAASNRCTPQGMSP 798

Query: 87 AKDKCKRSKSN-PPDPVNGMAHVIKDIOFGSQIKYSCPKGYRLIGSSSANCIIISGNTVI 145
A C+ RSC + +NG +H+Q+G++ + C +G+L GSS++ C++G +
Sbjct: 799 AAPCEVASCDDPMQQLNGRVLPVNIQLAKVDVCDGFOLGSSASVCLAGNESI 858

Query: 146 WDKTPVC 154
W++ PVC+
Sbjct: 859 WNSVPICE 867

Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFDQCNPEMLPAPARNLTDPEPIGTALNTECRPGYSGR-PSIIICLKNSWTSAXDKCKR 86
L S S C P + A T D P G +Y C PGT R S+ C W+
Sbjct: 290 LPSCSNVQPPDVLAERKTRD-RFSPQEVFISCEPGIDLRGAASNRCTPQGMSP 348

Query: 87 AKDKCKRSKSN-PPDPVNGMAHVIKDIOFGSQIKYSCPKGYRLIGSSSANCIIISGNTVI 145
A C+ RSC + +NG +H+Q+G++ + C +G+L GSS++ C++G +
Sbjct: 349 AAPCEVASCDDPMQQLNGRVLPVNIQLAKVDVCDGFOLGSSASVCLAGNESI 408

++ FG +Y+C +LIG S+ C GN V W + P C
Sbjct: 437 LEVFPFGKAVNYTCDDPHDRGTSFDLIGSTIRCTSDPQNGV-WSSPAARC 487

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTLYANECRPGY-----SGRPSTIIKSNWTSADKCRKSCNPPDPVNGMAHYKD 112
+G +++ C G S + + S+W S+ C++ C +P NG H K
Sbjct: 828 LGAKVDVFCDEGFOLGSSASACVLAQMSLVNCSVPCQIFCPSPVLENG-RHTCKP 886

Query: 113 IO--FGSQIKYSCP-----KGYRLIGSSATCII--SGNTVIMDKTPVC 153
++ FG +Y+C +LIG S+ C GN V W + P C
Sbjct: 887 LEVFPFGKAVNYTCDDPHDRGTSFDLIGSTIRCTSDPQNGV-WSSPAARC 937

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFARPTNLTDPF-----EPPIGYLANECRPGYSGRPF-----SIICLN-- 81
+P LP PT DF F G+ + Y C PG GR SI C N
Sbjct: 614 IPCGLP--PTIANGDFISTRENHFYGSVYTRCNPGSGRKFVELVGPSTICTSND 670

Query: 82 --SWTSADKCRKSCNPPDPVNGMAHYKD---IQFSQIKYSCPKGYRLIGSSA 135
+W+ +C + PP+ NG+ ++ D ++ C G+ + G
Sbjct: 671 QVGINSGAPQCIIPKCTPPEVNGI--LVSDNRSLFSLNVEVFRNQGFVNGRRV 728

Query: 136 TCIIISGNTVIMDKTPVC 153
C W+ + P C
Sbjct: 729 KCOALNK---WEPELPSC 743

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFARPTNLTDPF-----EPPIGYLANECRPGYSGRPF-----SIICLN-- 81
+P LP PT DF F G+ + Y C PG GR SI C N
Sbjct: 164 IFCGLP--PTIANGDFISTRENHFYGSVYTRCNPGSGRKFVELVGPSTICTSND 220

Query: 82 --SWTSADKCRKSCNPPDPVNGMAHYKD---IQFSQIKYSCPKGYRLIGSSA 135
+W+ +C + PP+ NG+ ++ D ++ C G+ + G
Sbjct: 221 QVGINSGAPQCIIPKCTPPEVNGI--LVSDNRSLFSLNVEVFRNQGFVNGRRV 278

Query: 136 TCIIISGNTVIMDKTPVC 153
C W+ + P C
Sbjct: 279 KCOALNK---WEPELPSC 293

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPIGYLANECRPGYSGRPF-----SIICLN-- 81
+P LP PT DF F G+ + Y C PG GR SI C N
Sbjct: 1792 DIFGKISIVACDHPRGNTFLIGSSIRCTSDPQNGVWSSPAFCESVPAACHP 1851

Query: 100 PDPNNG---AHVTKDIQFSQIKYSCPKGYRLIGSSAIIISGNTVIMDKTPVC 153
P NG HV + G I Y+C GY L+G C IW C
Sbjct: 1852 ERIQNGHYIGVNSLILP-GMTISTYCDPGLVNGKFICTMOG---TMSQDHYC 1904

Score = 36.7 bits (83), Expect = 0.12
Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PTNLTDPF-----EPPIGYLANECRPGYSGRPF-----SIICLN--SWTSAK 88
PT DF P GN + Y+C G G SI C WM+S

Sbjct: 1523 PTISNGPTSNRRTSFANGVTVYQCHFGDQGLFELVGRSTVCTSDQVWSSPP 1582

Query: 89 DKCRKSCNPPDPVNGMAHYKDIOFGSQ--IKYSCPKGYRLIGSSAIIISGNTV 145
+C + P+ N + V + P S I++ C G+ +G+ C +G
Sbjct: 1583 PCISTKCTAEPVENAL-RVPGNRSPSLTEIRRCQPGVWVSHVOCQYNGR-- 1638

Query: 146 WDKTPVC 153
W K P C
Sbjct: 1639 WGRPLHC 1646

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPTNLTDPEPIGYLANECRPGYSGRPSII-----CLK--NSV 83
C P +P R T + PP G +NY C P G P +I C N V
Sbjct: 421 CPSPPIYINRHRGKPLEV-PPFGKAVNYTCDDPHDRGTSFDLIGSTIRCTSDPQNGV 479

Query: 84 WTSADKCRK-RKSCNPPDPVNGMAHY---IKDIQFSQIKYSCPKGYRLIGSSAII 139
+S +C C+ P + D G+ +Y C Y S TC+
Sbjct: 480 WSSPAFCGLIGHCQAPDHFLPAKLTYQNASDPPIGTSIKTECRPEY-YGRPSITCL- 537

Query: 140 SGNTVIMDKTPVC 153
+ ++W + VC
Sbjct: 538 --DNVWSSPDVC 549

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPTNLTDPEPIGYLANECRPGYSGRPSII-----CLK--NSV 83
C P +P R T + PP G +NY C P G P +I C N V
Sbjct: 871 CPSPPIYINRHRGKPLEV-PPFGKAVNYTCDDPHDRGTSFDLIGSTIRCTSDPQNGV 929

Query: 84 WTSADKCRK-RKSCNPPDPVNGMAHY---IKDIQFSQIKYSCPKGYRLIGSSAII 139
+S +C C+ P + D G+ +Y C Y S TC+
Sbjct: 930 WSSPAFCGLIGHCQAPDHFLPAKLTYQNASDPPIGTSIKTECRPEY-YGRPSITCL- 987

Query: 140 SGNTVIMDKTPVC 153
+ ++W + VC
Sbjct: 988 --DNVWSSPDVC 999

>GSEQLAAV5751 Human C3b/C4b receptor (CRL) protein.
Length = 2039

Score = 256 bits (647), Expect = 8e-68
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLAALVLLISFS-DQCNVPEMLPFARPTNLTDPEPIGYLANECRPGYSGRPSI 76
G LLA +VLL + OCN PEMLPFARPTNLTD+PEPIGYLANECRPGYSGRPSI
Sbjct: 25 GSLAVVLLALPVAMGQNAPEMLPFARPTNLTDPEPIGYLANECRPGYSGRPSI 84

Query: 77 ICLKNSVWTSADKCRKSCNPPDPVNGMAHYKDIOFGSQIKYSCPKGYRLIGSSAII 136
ICLKNSVWTSADKCRKSCNPPDPVNGMAHYKDIOFGSQIKYSCPKGYRLIGSSAII
Sbjct: 85 ICLKNSVWTSADKCRKSCNPPDPVNGMAHYKDIOFGSQIKYSCPKGYRLIGSSAII 144

Query: 137 CIISGNTVIMDKTPVC 154
CIISG+TVIMDN+TP+CD
Sbjct: 145 CIISGNTVIMDKTPVC 162

Score = 176 bits (442), Expect = 9e-44
Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LLSFSDQCNVPEMLPPARPNTLTDPEPIGTLYANECRPGYSGRPYSIIICLNKSWTSAKDCKRK 87
LS + C PE PFA PT +DEFP+GT LNYECRPGY G+ PSI CL+N VM+S
Sbjct: 1389 LSVRAGHCKTEQEPFASPTIPIINDPEPIGTLYANECRPGYSGRPYSIIICLNKSWTSAKDCKRK 1448

Query: 88 KDCCKRSCRRPDPVNGMAHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTVIMDKRTPVCD 147
+D C+AKSC PP+P NCH H+ D OPGS + YSC +G+RLIG S TC++SGN V MD
Sbjct: 1449 EDCNRKSCGPPPEPFGNVAHNTDIOFGSVNCSNCHGRLIGSPRTIULVSGNNVYMD 1508

Query: 148 NKRPVCD 154
K P+C+

Sbjct: 1509 KKAIPCE 1515

Score = 166 bits (417), Expect = 8e-41
Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 35 CNVPEMLPPARPNTLTDPEPIGTLYANECRPGYSGRPYSIIICLNKSWTSAKDCKRK 94
C P+ PA+ T+ +PPIGT L YECRP Y GRPFSI CL N VM+S KD CKRK
Sbjct: 943 CQADHFLFARKLTQTNASDPPIGSLKRCRPYGRGPRSTICLDNLVMSPEKDCKRK 1002

Query: 95 SCRNPDVNGMAHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTVIMDKRTPVCD 153
SC+ PDPVNGM HVI DIQ GS+I YSC G+RLIG SSA CI+SGNT W R P+C
Sbjct: 1003 SCKTPDPVNGMAHVIKDIOGSRINYSCTGHRILIGSSAECILSGNTAHMSTKPPIC 1061

Score = 164 bits (412), Expect = 3e-40
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNVPEMLPPARPNTLTDPEPIGTLYANECRPGYSGRPYSIIICLNKSWTSAKDCKRK 94
C P+ PA+ T+ +PPIGT L YECRP Y GRPFSI CL N VM+S KD CKRK
Sbjct: 493 CQADHFLFARKLTQTNASDPPIGSLKRCRPYGRGPRSTICLDNLVMSPEKDCKRK 552

Query: 95 SCRNPDVNGMAHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTVIMDKRTPVCD 153
SC+ PDPVNGM HVI DIQ GS+I YSC G+RLIG SSA CI+SGN W R P+C
Sbjct: 553 SCKTPDPVNGMAHVIKDIOGSRINYSCTGHRILIGSSAECILSGNAHMSKTPIC 611

Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LLSFSDQCNVPEMLPPARPNTLTDPEPIGTLYANECRPGYSGRPYSIIICLNKSWTSAKDCKRK 86
L S S C P + A T D P G + Y C PGY R S+C W+
Sbjct: 740 LPSCSRVCOPPPDVLAERTORDK-NFSRQGVFYSCEPGYDLRGAASMCCTPQGMSP 798

Query: 87 AKDKCKRSCRRN-PDPVNGMAHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTVIMDKRTPVCD 145
A C+ KSC + NG ++O G+++ + C +G+L GSS++ C+++G +
Sbjct: 799 AAPCEVKSQCDPMQGLNGRVLPVNLQAKAVPDCDEGRLKSSASVCIAGNESL 858

Query: 146 WDKRTPVCD 154
W++ PVC+

Sbjct: 859 WMSVPVCE 867

Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LLSFSDQCNVPEMLPPARPNTLTDPEPIGTLYANECRPGYSGRPYSIIICLNKSWTSAKDCKRK 86
L S S C P + A T D P G + Y C PGY R S+C W+
Sbjct: 290 LPSCSRVCOPPPDVLAERTORDK-NFSRQGVFYSCEPGYDLRGAASMCCTPQGMSP 348

Query: 87 AKDKCKRSCRRN-PDPVNGMAHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTVIMDKRTPVCD 145
A C+ KSC + NG ++O G+++ + C +G+L GSS++ C+++G +
Sbjct: 349 AAPCEVKSQCDPMQGLNGRVLPVNLQAKAVPDCDEGRLKSSASVCIAGNESL 408

Query: 146 WDKRTPVCD 154

Sbjct: 409 WMSVPVCE 417
W++ PVC+

Score = 64.8 bits (155), Expect = 4e-10
Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)

Query: 28 LLSFSDQCNVPEMLPPARPNTLTDPEPIGTLYANECRPGYSGRPYSIIICLNKSWTSAKDCKRK 86
L S S C P + A T D P G + Y C PGY R S+C W+
Sbjct: 1190 LPSCSRVCOPPPDVLAERTORDK-NFSRQGVFYSCEPGYDLRGAASMCCTPQGMSP 1248

Query: 87 AKDKCKRSCRRNPDV-NGMAHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTVIMDKRTPVCD 145
+C KSC + +G ++O G+++ + C +G+L GSS + C++G +
Sbjct: 1249 EAPRCVNSCDDPLGQLPBGRVLPVNLQAKAVPDCDEGRLKSSVSHCVLGRSL 1308

Query: 146 WDKRTPVCD 154
W+N PVC+

Sbjct: 1309 WMSVPVCE 1317

Score = 61.3 bits (146), Expect = 5e-09
Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)

Query: 49 LTDDPEPIGTLYANECRPGYSGRPYSIIICLNKSWTSAKDCKRSCRRNPDV-NGMAHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTVIMDKRTPVCD 154
L+ F G + Y C P Y R S+C W+ +C KSC + +G
Sbjct: 1663 LSHQDFSPQGVFYSCEPSYDLRGAASLHCTPQGMSPDAPRCVNSCDDPLGQLPBGR 1722

Query: 107 AHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTVIMDKRTPVCD 154
+ ++O G+++ + C +G+L G S++ C+++G +W++ PVC+
Sbjct: 1723 VLPPLNLQAKAVPDCDEGRLKSSASVCIAGNESL 1770

Score = 48.0 bits (112), Expect = 5e-05
Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)

Query: 26 LLSFSDQCNVPEMLPPARPNTLTDPEPIGTLYANECRPGYSGRPYSIIICLNKSWTSAKDCKRK 79
L+ S S D C P PF ++ D +P G+ +N C G+ P S CL
Sbjct: 1443 LMSVSDNCRKSCGPPPEPFGNVAHNTDIOF--GSTVYNSCDEGRLIGSP-STYCL 1499

Query: 80 ---KNSVWTSADCKRCKRSCRRNPDVNGMAHVIKDIOF--GSOIKYSCPKGRLIGSSSANTCIISGNTVIMDKRTPVCD 158
N W W C+ SC PP NG + F G+ + Y C G +
Sbjct: 1500 VSGNNTVMDKAPVICHILICEPPTISNDPFSNNRSTFHNNTVTVYQCHTQDDEQLPFE 1559

Query: 129 LIGSSSANTCIISGNTVIMDKRTPVCD 158
L+G S C + V +W + P C S K
Sbjct: 1560 LVGRSIVCTSKDQYGVMSPPRCISTNR 1590

Score = 46.5 bits (108), Expect = 1e-04
Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)

Query: 57 IGTLYANECRPGYSGRPYSIIICLNKSWTSAKDCKRSCRRNPDVNGMAHVIKDIOF--GSOIKYSCPKGRLIGSSSANTCIISGNTVIMDKRTPVCD 154
+G ++++ C G+ GR S ++ ++W S+ C++ C NPP +NG
Sbjct: 1721 LGAKVFCVDEGRLKSSASVCIAGNESL 1790

Query: 111 KDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTVIMDKRTPVCD 154
DI +G +I Y+C + LIG SS C GN V W + P C+
Sbjct: 1791 GDIVYKEISYACVTHDRGNTVNLIGESSICTSDPGNGV-WSSAPVCE 1841

Score = 43.8 bits (101), Expect = 9e-04
Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)

Query: 58 GTLYANECRPGYSGRPYSIIICLNKSWTSAKDCKRSCRRNPDVNGMAHVIKDIOF--GSOIKYSCPKGRLIGSSSANTCIISGNTVIMDKRTPVCD 154
G ++Y C PGY G+ F I C ++ CR +C P +N+++ + K

Sbjct: 1870 GMTISVTCDPGLVVGKGF-IFCTDQIWSQDLHYCKEYVNSCFPLF-MNGISKELKHKV 1927

Query: 113 IQFGSQIKYSCPGY-----SGRPSTICLNKNSVWTSADKCKRCKSCNPPDPVNG--MAHYI 162

Sbjct: 1928 YHGDYVTLCKEDGYTLGSGFWSCQADR--WDPLAKCTSHADALI 1974

Score = 43.8 bits (101), Expect = 9e-04
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTYLVNTECRPGY-----SGRPSTICLNKNSVWTSADKCKRCKSCNPPDPVNG--MAHYI 111
+G +Y C GY S II +W + C R C PP NG ++
Sbjct: 124 GSOIKRSCYGRRLIGSSATCIIISGTYVWNERPFCIDRPGLPPTNGPSTNRE 183

Query: 112 DIQFGSQIKYSCPGK-----YRLIGSSATCIIISGNTV-IMDKTPVC 153
+GS +Y C G +L+G S C + + V IW P C
Sbjct: 184 NFHYGSVYTRCNPGSGGRKVELVGEPSIYCTSDNDQVIMSGAPQC 232

Score = 43.0 bits (99), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPPIGTYLVNTECRPGYS--GRPFSTICLNKNSV--WTSADKCKRCKSCNPPDPVNG--MAHYI 107
+G +NY C G+ G +L + W++ C+R C PP NG ++
Sbjct: 570 DIVGSRINYSCTGHRILIGHSAAECTLSGNAHNSKTPPICRILGCLPPTIANGDPTIS 629

Query: 108 HTIKDIQFGSQIKYSCPKG-----YRLIGSSATCIIISGNTV-IMDKTPVC 153
++ +GS +Y C G +L+G S C + + V IW P C
Sbjct: 630 TNRENHFYGSVYTRCNPGSGGRKVELVGEPSIYCTSDNDQVIMSGAPQC 682

Score = 43.0 bits (99), Expect = 0.002
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGTLYLVNTECRPGY-----SGRPSTICLNKNSVWTSADKCKRCKSCNPPDPVNG--MAHYI 110
+G +++ C G+ S ++ S+W ++ C+ C NP +NG
Sbjct: 1278 LGAKVFPVCEGRILKGSYSVHCVALGKRSIMNNSVPCVPEHIFCPVPEALINGHGTPTS 1337

Query: 111 KDIOFGSQIKYSCP-----KGYRLIGSSATCIIIS--GNTVIMDKTPVCDSK 158
DI +G +I Y+C +LIG S+ C GN V W + P C+ ++
Sbjct: 1338 GDIPYKREISYTCDDPHDPKGTNFIIGESTIRCTSDPHGNGV-WSPAPRCBLSVR 1392

Score = 42.6 bits (98), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPPIGTYLVNTECRPGYSGRFPS---ITCLNNSVWTSADKCKRCKSCNPPDPVNG--MA 107
+ +G +NY C G+ S I+ +W++ C+R C PP NG ++
Sbjct: 1020 DIVGSRINYSCTGHRILIGHSAAECTLSGNTAMSTKPIPCRIHCPPTIANGDPTIS 1079

Query: 108 HTIKDIQFGSQIKYSCPKG-----YRLIGSSATCIIISGNTV-IMDKTPVC 153
++ +GS +Y C G +L+G S C + + V IW P C
Sbjct: 1080 TNRENHFYGSVYTRCNLGSKRKVELVGEPSIYCTSDNDQVIMSGAPQC 1132

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTLYLVNTECRPGY-----SGRPSTICLNKNSVWTSADKCKRCKSCNPPDPVNGMAHYIKD 112
+G +++ C G+ S ++ S+W S+ C++ C +PP NG H K
Sbjct: 378 LGAKVFPVCEGRILKGSASVCLAGNESIMNNSVPCVCEQIFCPSPVPLNG-RHTKRP 436

Query: 113 IQ---FGSQIKYSCP-----KGYRLIGSSATCII--GNTVIMDKTPVC 153
++ FG +Y+C +LIG S+ C GN V W + P C
Sbjct: 437 LEVFPFGKAVNYTCDDPHDPKGTNFIIGESTIRCTSDPDGNGV-WSPAPRC 487

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTLYLVNTECRPGY-----SGRPSTICLNKNSVWTSADKCKRCKSCNPPDPVNGMAHYIKD 112
+G +++ C G+ S ++ S+W S+ C++ C +PP NG H K
Sbjct: 828 LGAKVFPVCEGRILKGSASVCLAGNESIMNNSVPCVCEQIFCPSPVPLNG-RHTKRP 886

Query: 113 IQ---FGSQIKYSCP-----KGYRLIGSSATCII--GNTVIMDKTPVC 153
++ FG +Y+C +LIG S+ C GN V W + P C
Sbjct: 887 LEVFPFGKAVNYTCDDPHDPKGTNFIIGESTIRCTSDPDGNGV-WSPAPRC 937

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLFPAPFNLTDDF-----EPPIGTYLVNTECRPGYSGRPF-----SITCLKN-- 81
+P LP PT DF F G+ +Y C PG GR SI C N
Sbjct: 614 IPGGLP---PTIANGDPISITNRENFHYGSVYTRCNPGSGGRKVELVGEPSIYCTSDND 670

Query: 82 --SVWTSADKCKRCKSCNPPDPVNGMAHYIKD---IQFGSQIKYSCPGYRLIGSSA 135
+W+ +C +C +P+ NG+ ++ D +++ C G+ + G
Sbjct: 671 QVGIMSGAPQCIIIPKCTPPVWENG--LVSDRSLFSLNVEVFCQPGYVMKGRPV 728

Query: 136 TCIIISGNTVIMDKTPVC 153
C W+ + P C
Sbjct: 729 KCOALNR---WEPPLPSC 743

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLFPAPFNLTDDF-----EPPIGTYLVNTECRPGYSGRPF-----SITCLKN-- 81
+P LP PT DF F G+ +Y C PG GR SI C N
Sbjct: 164 IPGGLP---PTIANGDPISITNRENFHYGSVYTRCNPGSGGRKVELVGEPSIYCTSDND 220

Query: 82 --SVWTSADKCKRCKSCNPPDPVNGMAHYIKD---IQFGSQIKYSCPGYRLIGSSA 135
+W+ +C +C +P+ NG+ ++ D +++ C G+ + G
Sbjct: 221 QVGIMSGAPQCIIIPKCTPPVWENG--LVSDRSLFSLNVEVFCQPGYVMKGRPV 278

Query: 136 TCIIISGNTVIMDKTPVC 153
C W+ + P C
Sbjct: 279 KCOALNR---WEPPLPSC 293

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPPIGTYLVNTECRPGYS--GRPSII-----NSVWTSADKCKRCKSCNPPDPVNG--MAHYI 99
+ P G +Y C G P++I C N W+S+ C+ +P
Sbjct: 1792 DIPYKREISYTCDDPHDPKGTNFIIGESTIRCTSDPDGNGVWSPAPRCBLSVR 1851

Query: 100 PDPVNG--AHYIKDIQFGSQIKYSCPKGGRRLIGSSATCIIISGNTVIMDKTPVC 153
P NG HV + G I Y+C GY L+G C G IW C
Sbjct: 1852 FRIQNGHYIGHNSLYLP-GMTISVTCDDPGLVVGKGFIFCTDQ--IMSQDLHYC 1904

Score = 36.7 bits (83), Expect = 0.12
Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PNTLNDP-----EPPIGTYLVNTECRPGYSGRPF-----SITCLKN--SVWTSAX 88
PT DF F GN +Y+C G G SI C W+S
Sbjct: 1523 PITSNGPYSNNRNSFHNHGVVYTCCHGPDGQLPELVGERSTIYCTSKDQGVWSSFP 1582

Query: 89 DRCKRSKNDPPVNGMAHVIKIDIOGSG---IKYSCPGRYLIGSSSANTCIISGNTVI 145
+C + P+ N+ V+ F S I++ C G+ ++G+ C +G
Sbjct: 1583 PRGISTNCTA PEVEENAI-RVGRNRSFSLTBIIRFCQSGRVAMGSHVQCQNGR--- 1638

Query: 146 WDKKTPVC 153
M K P C
Sbjct: 1639 WGRFLPHC 1646

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPNLTDDFEPIGYLYNECRPGYS-GRPSII-----CLK----NSV 83
C P +P R T + P P G +NY C P G F +I C N V
Sbjct: 421 CSPSPVBNRHTGKPLEV-FPRGKAVNYCDDPHDRGTSFDLIGSTIRCTSDPGNGV 479

Query: 84 WTSADCKR-RKSCNPPDPVNGMAHVIKIDIOGSGQIYSCPGRYLIGSSSANTCI 139
W+S +C C+ P + D G+ +NY C Y S TC+
Sbjct: 480 WSSPAFCGILGHQAPDHFLPAKLKTQYMASDPFGISLKYCRPEY-YGRPSITCL- 537

Query: 140 SGNVTYIMDKTPVC 153
+ ++W + VC
Sbjct: 538 --DNLWSSPKDVC 549

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPNLTDDFEPIGYLYNECRPGYS-GRPSII-----CLK----NSV 83
C P +P R T + P P G +NY C P G F +I C N V
Sbjct: 871 CSPSPVBNRHTGKPLEV-FPRGKAVNYCDDPHDRGTSFDLIGSTIRCTSDPGNGV 929

Query: 84 WTSADCKR-RKSCNPPDPVNGMAHVIKIDIOGSGQIYSCPGRYLIGSSSANTCI 139
W+S +C C+ P + D G+ +NY C Y S TC+
Sbjct: 930 WSSPAFCGILGHQAPDHFLPAKLKTQYMASDPFGISLKYCRPEY-YGRPSITCL- 987

Query: 140 SGNVTYIMDKTPVC 153
+ ++W + VC
Sbjct: 988 --DNLWSSPKDVC 999

>GSEQ:AAW73147 Amino acid sequence of the soluble complement
receptor 1 (sCR1).
Length = 778

Score = 256 bits (647), Expect = 8e-68
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLAALVLLLSFS-DQCNVPEMLPFARPNLTDDFEPIGYLYNECRPGYSGRPSI 76
G LLA +VLL + QCN PEMLPFARPNLTDDFEPIGYLYNECRPGYSGRPSI 89

Query: 30 GLLAVVLLALVAMGQCNAPFEMLPFARPNLTDDFEPIGYLYNECRPGYSGRPSI 89

Query: 77 ICLKNSWTSADCKR-RKSCNPPDPVNGMAHVIKIDIOGSGQIYSCPGRYLIGSSSANT 136
ICLKNSWWT AKD+C+RKSCNPPDPVNGM HVIK IDGSGQIYSC KGYRLIGSSSAT
Sbjct: 90 ICLKNSWTSADCKR-RKSCNPPDPVNGMAHVIKIDIOGSGQIYSCGYRLIGSSSAT 149

Query: 137 CIISGTYIMDKTPVC 154
CIISG+TYIMDK+TP+CD
Sbjct: 150 CIISGTYIMDKTPVC 167

Score = 164 bits (412), Expect = 3e-40
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNVPEMLPFARPNLTDDFEPIGYLYNECRPGYSGRPSIICLKNSWTSADCKR 94

Sbjct: 498 COADPHFLPAKLQYNASDPFGISLKYCRPEYGRPEPSITCLDNLWSSPKDCKR 557
C P+ FA+ T+ +PFIQ L YECR Y GRPSI CL N V+W S KD CKR

Query: 95 SCNRPDPVNGMAHVIKIDIOGSGQIYSCPGRYLIGSSSANTCIISGNTVI 153
SC+ PDPVNGM HVI DIQ GS+I YSC G+RLG SGA CI+SGN W R P+C
Sbjct: 558 SKRPPDPVNGMAHVIKIDIOGSRINYSCTGHLIGSSSANTCIISGMAHSTWTPIC 616

Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSPSQCNVPEMLPFARPNLTDDFEPIGYLYNECRPGYSGR-PSIICLKNSWTS 86
L S S C P + A T D F G + Y C FGR R S+ C W+
Sbjct: 295 LPSCSRVQPPEDVLAERTQDKD-WFSRQEVYSCPEGDVLGAASRPPQGDSP 353

Query: 87 AKDKCKRSKRN-PPDPVNGMAHVIKIDIOGSGQIYSCPGRYLIGSSSANTCIISGNTVI 145
A C+ KSC +NG +Q G+++ + C +G+LL GSS++ C++G +
Sbjct: 354 AAPCEVTSQDDFQGLNGRVLPVNLQGAKVDPVCDGRQLKSSASVYLAGMSL 413

Query: 146 WDKKTPVC 154
W++ PWC+
Sbjct: 414 WSSSPVCE 422

Score = 43.8 bits (101), Expect = 9e-04
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GRYLVNCRPRGY-----GRPSIICLKNSWTSADCKRSCNPPDPVNG--MAHVIK 111
G+ + Y C GY S II +W+ C R C P NG ++ +
Sbjct: 129 GSAIKYSCCKRYRLIGSSSANTCIISGTYIMDKTPVCICDIPGQLPPTIMGDFISTRE 188

Query: 112 DIQSGQIYSCPGK-----YRLIGSSSANTCIISGNTV-IMDKTPVC 153
+GS+ Y C G G +L+G S C + + V IW P C
Sbjct: 189 NFHYGSVYTRCNPDSGRKRVELWGEPSITCSNDQVGLMSGRAPQC 237

Score = 43.0 bits (99), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGYLYNECRPGYS--GRPSIICLKNSV--WTSADCKRSCNPPDPVNG--MA 107
+G+ +NY C G+ G + L + W++ C-R C P NG ++ +
Sbjct: 575 DIQGRINYSCTGHLIGSSSANTCIISGMAHSTWTPICQRIICGLPPTIANGDITS 634

Query: 108 HVIKIDIOGSGQIYSCPKG-----YRLIGSSSANTCIISGNTV-IMDKTPVC 153
++ +GS+ Y C G +L+G S C + + V IW P C
Sbjct: 635 TNRENFHYGSVYTRCNPDSGRKRVELWGEPSITCSNDQVGLMSGRAPQC 687

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTVIANECRPGY-----GRPSIICLKNSWTSADCKRSCNPPDPVNGMAHVIKID 112
+G + + + C G+ S + + + S+W S+ C++ C +P NG H K
Sbjct: 383 LKAKVDVCDDEFOUKSSASVYLAAGBSLWSSVPCQIQICSPVILNG-RHTKP 441

Query: 113 IQ---FSQIKYSCP-----KGYRLIGSSSANTCI--SGNTYIMDKTPVC 153
++ FG + Y+C +LIG S+ C GN V W + P C
Sbjct: 442 LEVFPKAVNYCDDPHDRGTSFDLIGSTIRCTSDPGNGV-WSSPAFC 492

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VEMLPFARPNLTDDFEPIGYLYNECRPGYSGRPF-----STICLN-- 81
+P LP FT DF F G+ + Y C PG GR ST C N

Subject: 169 IPGCLP---PTINMDPSTINRENFHYGSVTVYVNCNPGSGKXVFLVGEPSITVCTSDND 225
Query: 82 --SWTSAKDKCKRKSCNRPDPVNGMAHYTKD----IQFGSQIKYSCPKYGRLLIGSSSA 135
+M+ +C +C +P+ NG+ ++ D +++ C G+ + G
Subject: 226 QVGIWNGAPQCIIIPNKCTPPNVENGI--LVSDNRSLFSLNVEVFRQCPGVKMGPRRV 283
Query: 136 TCIISGNTVIMDKTPVC 153
C W+ + P C
Subject: 284 KCOALNK---WEPELPSC 298

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFARPNLTLDPE-----EPPIGTVLYNECRPGYSGRPFSII-----SIICLN-- 81
+P LP PT DP F G+ + Y C PG GR SI C N
Subject: 619 IPGCLP---PTINMDPSTINRENFHYGSVTVYVNCNPGSGKXVFLVGEPSITVCTSDND 675
Query: 82 --SWTSAKDKCKRKSCNRPDPVNGMAHYTKD----IQFGSQIKYSCPKYGRLLIGSSSA 135
+M+ +C +C +P+ NG+ ++ D +++ C G+ + G
Subject: 676 QVGIWNGAPQCIIIPNKCTPPNVENGI--LVSDNRSLFSLNVEVFRQCPGVKMGPRRV 733
Query: 136 TCIISGNTVIMDKTPVC 153
C W+ + P C
Subject: 734 KCOALNK---WEPELPSC 748

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPNLTLDPEPIGTVLYNECRPGYS-GRPFSII-----CLK-----NSV 83
C P +P R T + PP G +NY C P G +T C N V
Subject: 426 CSEPPVYINGRHTRGKFLXY-FPGKAVNTCTDPHPRGRISFDLIGSTRICTSDPQNGV 484
Query: 84 WTSANDKCK-RKSCNRPDPVNGMAHY--IKDIQFGSQIKYSCPKYGRLLIGSSSARCI 139
W+S +C C+ P + D G+ +X C Y S TC+
Subject: 485 WSSPAFRGCIIGHCQAFHFLAKLTQTNASDPITSLAKYECRPRY-YGRPFSICTL- 542
Query: 140 SGNVTIWMNKTPVC 153
+ +W + VC
Subject: 543 --DNWSSPQDVC 554

>GSEQ:MAR11810 Human complement type 1 receptor.
Length = 2039

Score = 256 bits (647), Expect = 8e-68
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLLAALVLLISFS-DQCNPEMLPFARPNLTLDPEPIGTVLYNECRPGYSGRPFSI 76
G LLA +VL + QCN PEMLPFARPNLTLD+PEPIGTVLYNECRPGYSGRPFSI
Subject: 25 GSLIAVVLLALPVAMGQCNAPEMLPFARPNLTLDPEPIGTVLYNECRPGYSGRPFSI 84
Query: 77 ICLKNSWTSANDKCKRKSCNRPDPVNGMAHYTKDIQFGSQIKYSCPKYGRLLIGSSSAR 136
ICLKNSWTF AKD+C+RKSCNRPDPVNGM HVK IQFGSQIYSC KGRLLIGSSSAR
Subject: 85 ICLKNSWTSANDKCKRKSCNRPDPVNGMAHYTKDIQFGSQIKYSCPKYGRLLIGSSSAR 144
Query: 137 CIIISGNTVIMDKTPVC 154
CIIISG+TIVMDN+TP+CD
Subject: 145 CIIISGNTVIMDKTPVC 162

Score = 176 bits (442), Expect = 9e-44
Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LSSFDQCNPEMLPFARPNLTLDPEPIGTVLYNECRPGYSGRPFSIIICLNKNSVWTS 87
LS +C PE PPA PT +PEP+NGT INYERROY G PSI CLN VM+S
Subject: 1389 LSVNAGCKTFEQPPASPTIINDPEPIGTVLYNECRPGYSGRPFSIIICLNKNSVWTS 1448
Query: 88 KDKCKRKSCNRPDPVNGMAHYTKDIQFGSQIKYSCPKYGRLLIGSSSARCIISGNTVIM 147
+D C+RSC PP+P NGM H+ D QFGS + YSC +G+RLIGS S TC++SGN V WD
Subject: 1449 EBNCRKRSQPPPEPFGMVHINTVQFGSTVNSCNEGRLLIGSPTVCLVSGNNVTMD 1508
Query: 148 NKTPVCD 154
K P+C+
Subject: 1509 KKAPICE 1515

Score = 166 bits (417), Expect = 8e-41
Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 35 CNVPEMLPFARPNLTLDPEPIGTVLYNECRPGYSGRPFSIIICLNKNSVWTSANDKCKRK 94
C P+ PA+ T+ +PEPIT L YECRP Y GRPFSI CL N VM+S KD CKRK
Subject: 943 COADPHFLAKLTQTNASDPITSLAKYECRPRYGRPFSICTLNDLWSSPQDVCXK 1002
Query: 95 SCNRPDPVNGMAHYTKDIQFGSQIKYSCPKYGRLLIGSSSARCIISGNTVIMDKTPVC 153
SC+ PDPVNGM HVI DIQ GS+I YSC +G+RLIG SSA CI+SGNT W R P+C
Subject: 1003 SKCTPPDPVNGMAHYTKDIQVGSINTCTTGRLLIGHSSAECTLLSGNTAHMSTKPPIC 1061

Score = 164 bits (412), Expect = 3e-40
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNVPEMLPFARPNLTLDPEPIGTVLYNECRPGYSGRPFSIIICLNKNSVWTSANDKCKRK 94
C P+ PA+ T+ +PEPIT L YECRP Y GRPFSI CL N VM+S KD CKRK
Subject: 493 COADPHFLAKLTQTNASDPITSLAKYECRPRYGRPFSICTLNDLWSSPQDVCXK 552
Query: 95 SCNRPDPVNGMAHYTKDIQFGSQIKYSCPKYGRLLIGSSSARCIISGNTVIMDKTPVC 153
SC+ PDPVNGM HVI DIQ GS+I YSC +G+RLIG SSA CI+SGN W K P+C
Subject: 553 SKCTPPDPVNGMAHYTKDIQVGSINTCTTGRLLIGHSSAECTLLSGNTAHMSTKPPIC 611

Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFDQCNPEMLPFARPNLTLDPEPIGTVLYNECRPGYSGR-PEFSIIICLNKNSVWTS 86
L S S C P + A T D F G + Y C PGY R S+ C W+
Subject: 740 LPSCSRVCOPEPDLHAKRTQDKD-NFSPQEVYFSCPEGIDLGAMASRCYPOQDMSP 798
Query: 87 AADCKRKSCRN-PDPVNGMAHYTKDIQFGSQIKYSCPKYGRLLIGSSSARCIISGNTV 145
A C+ KSC + +NG ++Q G+++ + C +G++L GSS++ C+++G +
Subject: 799 AAPTEVYSCDDPMQQLNGRVLPVNIQLGAKVDCDEGFLKSSASVCLVAGWESL 858
Query: 146 WDKTKPVCD 154
W++ PVC+
Subject: 859 WNSVFPCE 867

Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFDQCNPEMLPFARPNLTLDPEPIGTVLYNECRPGYSGR-PEFSIIICLNKNSVWTS 86
L S S C P + A T D F G + Y C PGY R S+ C W+
Subject: 290 LPSCSRVCOPEPDLHAKRTQDKD-NFSPQEVYFSCPEGIDLGAMASRCYPOQDMSP 348
Query: 87 AADCKRKSCRN-PDPVNGMAHYTKDIQFGSQIKYSCPKYGRLLIGSSSARCIISGNTV 145
A C+ KSC + +NG ++Q G+++ + C +G++L GSS++ C+++G +
Subject: 349 AAPTEVYSCDDPMQQLNGRVLPVNIQLGAKVDCDEGFLKSSASVCLVAGWESL 408
Query: 146 WDKTKPVCD 154

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

W++ PVC+
Sbjct: 409 WNSSVPVCE 417

Score = 64.8 bits (155), Expect = 4e-10
Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)

Query: 28 LSFSDQCNVPELPLPAFTNLTDDEPPIGTYLNTBCRPGISGR-PFSLICLKNSVMTS 86
L S S C P + T D F G + Y C PGY R S+ C W+
Sbjct: 1190 LPSCSRVCQPPPEILHGETPSSHQD-NFSPQGEVVFSCPEGYDLRGAASLHCTPQGDWSP 12

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Query: 87  AADCKCRKSCSNPPDV-NGMAHVTKDIOFGSQIKYSPCKGRILIGSSATCIISNTVI 145
          +C KSC + +G ++Q+++ C +G+L GSS +C+ G +
Sbjct: 1249 EAPRCAYKSCDPLGQLPHGRVLPPLNTLQGAKYSPVCDGFRLLKSSSVSHCVLVGNRSL 1308

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Query: 146 WDNKTPVCD 154
        W+N PVC+
Sbjct: 1309 WNNSPVCE 1317
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Score = 61.3 bits (146), Expect = 5e-09
Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)

Query: 49 LTTDFEPIGNYLNTCRPGYSGR -PFSITCLKNLSVWMSAKDKCRKRSRNPDPF-NGM 106
L+ P G + Y C P Y R S+ C W+ +C KSC + + +G
Sbjct: 1663 LSHQDNFSPQGEVYFVSCFPTDLRGAASLCHCTPGQDWSPEAPRCTVYKSCDDFLGQLPHGR 1722

Query: 107 AHVIKDQFGSQIKYISCEPKGYRLIGSSATCIISGTVIMDNKTPVCD 154
+ ++Q g+++ C +G+RL G S++ C+++ +W++ PVC+
Sbjct: 1723 VLLPLNTQIGAKVSPVCEDEGFRLLKGRSASHCVTLAGKALMNSSVPCE 1770

Score = 48.0 bits (112), Expect = 5e-05
Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)

Query: 26 LLLSFFSDQCNV-----PEMLPFRPTNLVDDEPPIGTYLANTYCRPGS--GRPFILICL 79
L+ SS D C P PF ++ D +F G+ +NY C G+ G P S CL
Sbjct: 1443 LTVSSVEDNCRRKSCGPPEPFGNGVHINTDYP--GSTVNTSCNKGRLIGSP-STTCL 1499

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Query: 80  ---KNSWTSAKDKCKARKSCRNPPVNGAHVAKIDIF--GQIKKSCPKG-----YR 128
          N W      C + SC  PP  NG  +      F  G + + Y C  G      +
Sbjct: 1500 VGNNTWWDKAKAPICETIISCPEPPITSNQDFYSNNRTSFHNGIVVTYQCHNGPDGEQLFE 1555

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Query: 129 LIGSSATCIIISWT-VIWDNKTPTCDSELK 158
L+G S C + V +W + P C S K
Sbjct: 1560 LVGRSITCTSDKDQVGWSSPPRCISTNK 1590

Score = 46.5 bits (108), Expect = 1e-04
Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)

Query: 57 IGYLYANTECRGQY--SGRPFSS--IICLKNSVWTFSAKDCKRKSRCRNPDPVNG--NAHVI 110
+G +++ C G+ GR S ++ ++W S+ C++ C NRP +NG
Sbjct: 1731 LGAKSVFVCDGEGFRLKGRSASHCVLAGMALMNSVVPVCEQITFCPNPDAILNGRHGTGP 1790

Query: 111 KDIQEGSQIKRSCP-----KGYRLISSSATCII--SGNTYIMDNKPTPCD 154
 DI +G +I Y+C +LIG SS C GN V W + P C+
 Sbjct: 1791 GDIPYKEISYACDTHPDREKTFNLIGESSIRCTSDPGNGV-WSSPADPCE 1844

Score = 43.8 bits (101), Expect = 9e-04
Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)

Query: 58 GFLNTECRPGYS--GRPFSTICLNKNSVWTSJAKDKCRKRSCKRNPDPVNGMAHTI---KD 112
G ++Y C PGY G+ F I C ++ CK +C P +NG++ + K

Subject: 1870 OTTISTYOCPGYIALVKGXF-IPCTOTOGIWSQDHYCKEVCNCSPLPJ-ANGISKELENTKY 1922
 Query: 113 IOFGSGHKVSCPCRGYLTIGSSATCISGNTVIMDCKFPVDCSFLAPL 162
 + G + C GY L G S + C
 Subject: 1928 YHVEDYVTLKCEBDYLTLESGFMSGCCQDDR---WDPLAKTSTSAHDHAI 1974

Score = 43.8 bits (101), Expect = 9e-04
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GYLATTECRAGY-----SGAPFSLICLKNSWTSKDKCKRKSCLNPDPVNG--MAHVIK 1111
G+ + Y C GY S II +W + C R C P P NG ++ +
Sbjct: 124 GSGIHYSCCTGTYRLIGSSSATCIISGDTVIWINDNETPICDRIPCLGLPPTINGDFISTWRE 1633

Query: 112 DIQFGSQIKYSCPKG-----YRLIGSSSATCIIISGNTV-IWDNKTPTVC 153
 + +GS + Y C G + L+G S C + + V IW P C
 Sbjct: 184 NFHYGSVVTYRCNPFSGGGRKYFELVGEPSIYCTSNDDQVGVIWSGPAPOC 232

Score = 43.0 bits (39), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTYINTEYCKPGYS--GRPSIILKNV--WMSAKDCRKRSCRNEDDPVNG--MA 107
 + +G+ +NY C G+ G + L + W++ C+R C PP NG ++
 Sbjct: 570 DIOVGRINYSCTTGHKLIGHSSACILSGNAAHMSTKPPICQRIPCGLPPTIANGDFIS 629

Query: 108 HVKIDIGESQIKRSCPKG-----YRLIGSSATCIIISGTV-IWDNKTPVC 15
 ++ +GS + Y C G + L+G S C + + V IW P C
 Sbjct: 630 TNRENPHYGSVVTYACNPNPGSGGRKVFELVGEPSIYCTSNDDQVGIMSGAPQC 68

Score = 43.0 bits (9%), Expect = 0.002
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGYLTNTECRPGV----SGRPSIILKNSVWTSADKCRKRSKNPDPVNG--MAHYI 110
 +G +++ C G+ S ++ S+W ++ C+ C NPP +NG
 Sbjct: 1278 LGAKVSFVCDGEGRFLKSSVSHCVLTGMRSLMNNSVPVCEHIFCPNPAILNGRHTGPS 133

Query: 111 KDIFOSQIKRSCP-----KGRLLIGSSATCLIS--GNTVINDNKTPTVCDSELR 158
DI +G +I Y+C + LIG S+ C GN V W + P C+ ++
Sbjct: 1338 GDIPYKKEISYTCDDPHDRGMPTNLIGESTIRCTSDPHNGV--WSSPAFRCESLR 139

Score = 42.6 bits (98), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EEPIGTFLANTSCRPVSGSRFP-----ILKNSVWTSADKCKRKSQNPDPVNG--MA.107
+ +G+ +NY C G+ S I+ +W++ C+R C PP NG ++
Sbjct: 1020 DIQVGSINVCYTGHRLLGHSSAECILSGNTIAHWSTKPPICORIPGGLPPIIANDPFI 1079

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Query: 108  HVINDIQFGSLKRYSCPKG-----YRLIGSSATCIISGNTV-IMDNKTPVC 153
          ++  +GS + Y C G      + L+G S C + + V IW      P C
Sbjct: 1080  TNRENPHYGSVVTYRCNLASGRKRVPELVGEPSIYCTSNDDQVGIMSGPAPOC 113

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Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTVINTECRPGY----SRRPFSITCLNKSVMNFSARKDKRKRSRNPDPVNGAAHVTKD 112
+G +++ C G+ S ++ S+W S+ C++ C +PP NG H K
Sbjct: 378 LGAAYDFVCDDEGFQULKGSSASVYLAIGMSLNNSSVPVCEQIFCPSPVPIPG-N-RHTGKP 436

Query: 113 IQ---FGSQRKSCP-----KGYRLIGSSSANCII--SGATVIMDKNTPVC 153
 ++ FG + Y+C + LIG S+ C GN V W + P C
 Sbjct: 437 LEVPPFGKAVNVTCDPHDPRTGSFDLIGESTINCTSDPGNGV-WSSAPRC 487

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTATLNECHPQY-----SGRPSITLKNVWTSKCKRSCRNPPDVGMAHVIKD 112
+G +++ C G+ S ++ S+W S+ C++ C +PP NG H R
Sbjct: 828 LQAKVDVCDGEGQLKGSASVCVLAEGSLNASSVPCQJFCSPPEVLENG-RHNGAF 886

Query: 113 IQ---FGSQIKYSCP-----KGYRLIGSSSANCII--SGNTVIMDKRTVPC 153
++ FG + Y+C + LIG S+ C GN V W + P C
Sbjct: 887 LEVFPFGKAVNYTCDPHDRGTSFDLIGESTRICTSDPQNGV-WSPAPARC 937

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPENLFPARPTNLTDDF-----EPPIGTVLYNECRPGYSGRPF-----SIICLN-- 81
+P LP PT DF F G+ + Y C PG GR SI C N
Sbjct: 614 IFQGLP---PTIANGDFISTNEENHYGVVYTRCNGSGKRVFELVGPESITCTSDND 670

Query: 82 --SWTSADKCK-RKSCRNPPDVGMAHVIKD---IQFGSQIKYSCPKGYRLIGSSSANCII 135
+W+ +C + PP+ NG+ ++ D
Sbjct: 671 QVGIWSPAPQCIIPNCKCTPENVNGI--LVSDNNSLFLSINEVVEFGQPGFVAKGRNV 728

Query: 136 TCIISGNTVIMDKRTVPC 153
C W+ + P C
Sbjct: 729 KQALNR---WEPELPSC 743

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPPIGTVLYNECRPGYSGRPSII-----CLK-----NSWTSADKCKR--SCNP 99
+P G +Y C G P+I C N WWS+ C+P
Sbjct: 1792 DIFGKEISYACDHPRGATPNDIGESINCTSDPQNGWSPAPRCHELVSVAACRHF 1851

Query: 100 PDVNGH---AHVTKDIQFGSQIKYSCPKGYRLIGSSSANCIIISGNTVIMDKRTVPC 153
P NG HV + G I Y+C GR L+G C G IW C
Sbjct: 1852 PRLONGHYIGHVSLLP-GMTISYCDPGYLLVKGPIFCTDQ--IWSQLDHYC 1904

Score = 36.7 bits (83), Expect = 0.12
Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PTNLTDDF-----EPPIGTVLYNECRPGYSGRPF-----SIICLN--SWTSAX 88
PT DF F GT + Y+C G G SI C W+S
Sbjct: 1523 PTISNGDFYSNNRTSFPNGTGVYVYCHTGPDBOLFELVGERSTYCTSKDQVWSSPP 1582

Query: 89 DCKRKSCHNPPDVGMAHVIKDQFGSQ--IKYSCPKGYRLIGSSSANCIIISGNTV 145
+C + P+ N + V + P S I++ C G+ ++GS + C +G
Sbjct: 1583 PRCISNKTGADEVENAI-RVNGRSPFLTEIRFCQPGFVAVGSHVQCQTNR-- 1638

Query: 146 WDKRTVPC 153
W K P C
Sbjct: 1639 WGRPLPHC 1646

Score = 34.0 bits (76), Expect = 0.76
Identities = 33/138 (23%), Positives = 50/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPENLFPARPTNLTDDF-----EPPIGTVLYNECRPGYSGRPF-----SIICLN-- 81
+P LP PT DF F G+ + Y C PG GR SI C N
Sbjct: 164 IFQGLP---PTIANGDFISTNEENHYGVVYTRCNGSGKRVFELVGPESITCTSDND 220

Query: 82 --SWTSADKCK-RKSCRNPPDVGMAHVIKD---IQFGSQIKYSCPKGYRLIGSSSANCII 135
+W+ +C + PP+ NG+ ++ D
Sbjct: 221 QVGIWSPAPQCIIPNCKCTPENVNGI--LVSDNNSLFLSINEVVEFGQPGFVAKGRNV 278

Query: 136 TCIISGNTVIMDKRTVPC 153
C W+ + P C
Sbjct: 279 KQALNR---WEPELPSC 293

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLFPARPTNLTDDFEPPIGTVLYNECRPGYSGRPSII-----CLK-----NSV 83
C P +P R T + PP G +Y C P G P +I C N V
Sbjct: 421 CSPPPIVINGRHRGRPLEV-FPGGAVNYTCDPHDRGTSFDLIGESTRICTSDPQNGV 479

Query: 84 WTSADKCK-RKSCRNPPDVGMAHVIKD---IQFGSQIKYSCPKGYRLIGSSSANCII 139
W+S +C C+ P + D G+ +KY C Y S TC+
Sbjct: 480 WSPAPRCGILGHCOAPDHPFLAKIQTWASDPFGISLAKYCRPEY-YGRPSITCL- 537

Query: 140 SGNTVIMDKRTVPC 153
+ ++W + VC
Sbjct: 538 --DNLWMSPEPVC 549

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLFPARPTNLTDDFEPPIGTVLYNECRPGYSGRPSII-----CLK-----NSV 83
C P +P R T + PP G +Y C P G P +I C N V
Sbjct: 871 CSPPPIVINGRHRGRPLEV-FPGGAVNYTCDPHDRGTSFDLIGESTRICTSDPQNGV 929

Query: 84 WTSADKCK-RKSCRNPPDVGMAHVIKD---IQFGSQIKYSCPKGYRLIGSSSANCII 139
W+S +C C+ P + D G+ +KY C Y S TC+
Sbjct: 930 WSPAPRCGILGHCOAPDHPFLAKIQTWASDPFGISLAKYCRPEY-YGRPSITCL- 987

Query: 140 SGNTVIMDKRTVPC 153
+ ++W + VC
Sbjct: 988 --DNLWMSPEPVC 999

>GSEQ:AAFP2219 CRI protein.
Length = 2317

Score = 256 bits (647), Expect = 8e-68
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLI1AALTLISFS-DOCVPEMLFPARPTNLTDDFEPPIGTVLYNECRPGYSGRPSII 76
G LIA +VIL + QCN PEMLFPARPTNLTDDFEPPIGTVLYNECRPGYSGRPSII
Sbjct: 34 GSILAVVLLALFVAMQCNAPMLFPARPTNLTDDFEPPIGTVLYNECRPGYSGRPSII 93

Query: 77 ICLKNSWTSADKCK-RKSCRNPPDVGMAHVIKDQFGSQIKYSCPKGYRLIGSSSANCII 136
ICLKNSWTF AKD+C+RSCRNPPDVGMAHVIK IQFGSQIKYSC KGYRLIGSSSANCII
Sbjct: 94 ICLKNSWTSADKCK-RKSCRNPPDVGMAHVIKIQFGSQIKYSCPKGYRLIGSSSANCII 153

Query: 137 CIISGNTVIMDKRTVPC 154
CIISG+TVIMDN+TP+CD
Sbjct: 154 CIISGNTVIMDKRTVPC 171

Score = 176 bits (442), Expect = 9e-44
Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LSSSDQCNVPEMLFPARPTNLTDDFEPPIGTVLYNECRPGYSGRPSIIICLKNSWTSAX 87
LS + C PE PPA PT +DEPP+GT LNECHPQY G+ FSI CLK+ W+S

Subject: 1398 LSVAGHCKTEBPQFPAFTPIRINDEFPVGTSLNTECRPGYFGKMFSTICLENLWMSV 1457
Query: 88 KDKCKRSCRNPPDPVNGAHVINDIQFSGQIKYSCPKGRLIGSSSACIIISGNTVMD 147
+D+KRSK PP+P NGM H+ D QFGS + YSC +G+RLIGS S TC++SGN V MD
Subject: 1458 EDNCRKSCGPEPFNGVHINTDIQFSGTVNSCNEGRLIGSSTTCIIVSGNVMD 1517
Query: 148 NKTPVCD 154
K P+C+
Subject: 1518 KKAPICE 1524
Score = 166 bits (417), Expect = 8e-41
Identities = 75/119 (63%), Positives = 85/119 (71%)
Query: 35 CNVEMLPPARPTNLTDPEPIGTLYNTECRPGYSGRPSTICLNKSWTSADKCKR 94
C P+ FA+ T+ +PIGT L YECRP Y GRPST CL N VM+S KD CKR
Subject: 952 CQADHFLFAKLTQTNASDPFIOTSLKTECRPEYGRPSTICLDNLVMSRPDVCCKR 1011
Query: 95 SCRPDPVNGAHVINDIQFSGQIKYSCPKGRLIGSSSACIIISGNTVMDNKTPVC 153
SC+ PDPVNGM HVI DIQ GS+I YSC G+RLIG SSA CI+SGN W K P+C
Subject: 1012 SCRPDPVNGAHVINDIQGSRINSCCTGRLIGSSACIIISGNTVMDNKTPVC 1070
Score = 164 bits (412), Expect = 3e-40
Identities = 74/119 (62%), Positives = 84/119 (70%)
Query: 35 CNVEMLPPARPTNLTDPEPIGTLYNTECRPGYSGRPSTICLNKSWTSADKCKR 94
C P+ FA+ T+ +PIGT L YECRP Y GRPST CL N VM+S KD CKR
Subject: 502 CQADHFLFAKLTQTNASDPFIOTSLKTECRPEYGRPSTICLDNLVMSRPDVCCKR 561
Query: 95 SCRPDPVNGAHVINDIQFSGQIKYSCPKGRLIGSSSACIIISGNTVMDNKTPVC 153
SC+ PDPVNGM HVI DIQ GS+I YSC G+RLIG SSA CI+SGN W K P+C
Subject: 562 SCRPDPVNGAHVINDIQGSRINSCCTGRLIGSSACIIISGNTVMDNKTPVC 620
Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)
Query: 28 LLSFSDQCNVPEMLPPARPTNLTDPEPIGTLYNTECRPGYSGR-PFSTICLNKSWTS 86
L S S C P + A T D F G + Y C PGY R S+C W+
Subject: 749 LSCSRVCOPEPDLHAERTORDND-NFSQGEVYSCPEYGRPSTICLDNLVMSRPDVCCKR 807
Query: 87 AKDKKRSKRN-PPDPVNGAHVINDIQFSGQIKYSCPKGRLIGSSSACIIISGNTV 145
A C+ KSC + NG ++Q G+++ + C +G+RL GSS++ C+++ +
Subject: 808 AAPTEVYSCDDPFNGQLNGRVLPVNLQGAKVDFVCEGQLKSSASVCLAGMESL 867
Query: 146 WDKTPVCD 154
W+N P+C+
Subject: 868 WNSVFPCE 876
Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)
Query: 28 LLSFSDQCNVPEMLPPARPTNLTDPEPIGTLYNTECRPGYSGR-PFSTICLNKSWTS 86
L S S C P + A T D F G + Y C PGY R S+C W+
Subject: 299 LSCSRVCOPEPDLHAERTORDND-NFSQGEVYSCPEYGRPSTICLDNLVMSRPDVCCKR 357
Query: 87 AKDKKRSKRN-PPDPVNGAHVINDIQFSGQIKYSCPKGRLIGSSSACIIISGNTV 145
A C+ KSC + NG ++Q G+++ + C +G+RL GSS++ C+++ +
Subject: 358 AAPTEVYSCDDPFNGQLNGRVLPVNLQGAKVDFVCEGQLKSSASVCLAGMESL 417
Query: 146 WDKTPVCD 154
W+N P+C+
Subject: 418 WNSVFPCE 426

Score = 64.8 bits (155), Expect = 4e-10
Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)
Query: 28 LLSFSDQCNVPEMLPPARPTNLTDPEPIGTLYNTECRPGYSGR-PFSTICLNKSWTS 86
L S S C P + A T D F G + Y C PGY R S+C W+
Subject: 1199 LSCSRVCOPEPDLHAERTORDND-NFSQGEVYSCPEYGRPSTICLDNLVMSRPDVCCKR 1257
Query: 87 AKDKKRSKRNPPDPV-NGAHVINDIQFSGQIKYSCPKGRLIGSSSACIIISGNTV 145
+C KSC + NG ++Q G+++ + C +G+RL GSS + C++ G +
Subject: 1258 BAPCAVNSCDDPFLQGLPHGRVLPVNLQGAKVDFVCEGQLKSSASVCLAGMESL 1317
Query: 146 WDKTPVCD 154
W+N P+C+
Subject: 1318 WNSVFPCE 1326
Score = 61.3 bits (146), Expect = 5e-09
Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)
Query: 49 LTDDPEPIGTLYNTECRPGYSGR-PFSTICLNKSWTSADKCKRSCRNPPDPV-NGM 106
L+ F G + Y C P Y R S+C W+ +C KSC + +G
Subject: 1672 LSHODNFSQGEVYSCPEYGRPSTICLDNLVMSRPDVCCKR 1731
Query: 107 AHVINDIQFSGQIKYSCPKGRLIGSSSACIIISGNTVMDNKTPVC 154
+ ++Q G+++ + C +G+RL G S++ C+++ W++ P+C+
Subject: 1732 VLLPMLQGAKVDFVCEGQLKSSASVCLAGMESL 1779
Score = 48.0 bits (112), Expect = 5e-05
Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)
Query: 26 LLSFSDQCNVPEMLPPARPTNLTDPEPIGTLYNTECRPGYSGR-PFSTICLNKSWTS 79
L+ S S D C P PF ++ D +F G+ +NY C G+ G P S CL
Subject: 1452 LMSVENDCKRSCGPEPFNGVHINTDIQF-GSTVYSCNEGRLIGSP-STYCL 1508
Query: 80 ---NNSVTSADKCKRSCRNPPDPVNGAHVINDIQF-GSQIKYSCPKG-----YR 128
N W C+ SC PP NG + F G+ + Y C G
Subject: 1509 VSGNVTWMDKAPICELISCEPPTISNGDVFSGNNTSFGHGTVTYQCHTGDDBOLFE 1568
Query: 129 LIGSSSACIIISGNTV-IMDKTPVCDSELK 158
L+G S C + V W+ + P C S K
Subject: 1569 LVGRSIVCTSKDQVGVMSPPRCISTNRK 1599
Score = 46.5 bits (108), Expect = 1e-04
Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)
Query: 57 IGTLYNTECRPGYSGRPFPS-IICLNKSWTSADKCKRSCRNPPDPVNG-MAHVI 110
+G +++ C G+ GR S ++ ++W S+ C++ C NP+ +NG
Subject: 1740 LGANVFPVCEGQLKSSASVCLAGMESLWNSVFPCEGQICPPEPALINRHTGTPP 1799
Query: 111 KDIOFSGQIKYSCPKGRLIGSSSACIIISGNTVMDNKTPVC 154
DI +G +Y +C + LIG SS C GN V W + P C +
Subject: 1800 GDIVYKREIYACDHPDNGMTNMLGSSSIRCTSDPQANV-WSSPAPICE 1650
Score = 43.8 bits (101), Expect = 9e-04
Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)
Query: 58 GTVYNTYECRPGYSGRPFSTICLNKSWTSADKCKRSCRNPPDPVNGAHVIT--KD 112
G +Y C PGY G+ F I C W+ CK +C P +NG++ + K
Subject: 1879 GMTIYSTCDPGVYLVGKGF-IFCTDGIWISQDLHCKREYVNSPFLP-INGISLEKAKV 1936

Query: 113 IQFGSQRKSCPRGYRLIGSSAATCIIISGNTVIMDKKTPVCDSELYAFLL 162
+G + C GY L GS + C MD C S A +
Sbjct: 1937 YHGGDYVTLKCEGDTYTLGSPWISGQCAADR---WDPEPLAKCTSHADAL 1983

Score = 43.8 bits (101), Expect = 9e-04
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTVLANTECRPGY----SGRPSIICLNKSVMTSADCKRKSRRNPDPVNG--MAHYIK 111
G+ + Y C GY S II +W + C R C PP NG ++ +
Sbjct: 133 GSQIKYSCCTGRLIGSSAATCIIISGNTVIMDKKTPVCDSELYAFLL 192

Query: 112 DIOFGSQRKSCPRG-----YRLIGSSAATCIIISGNTVIMDKKTPVC 153
+ +G S + Y C G + L+G S C + + V IW P C
Sbjct: 193 NPHGSVVYTRCNPGSGRKFELVGPSPITCTSDPDQGVMSGAPPC 241

Score = 43.0 bits (99), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTYLANTECRPGYS--GRPSIICLNKSV--WTSADCKRKSRRNPDPVNG--MA 107
+ +G + NY C G+ G + L + M+ + C R C PP NG ++ +
Sbjct: 579 DIOGSRINYSCTGRLIGSSAATCIIISGNTVIMDKKTPVCDSELYAFLL 638

Query: 108 HVIKDIQFGSQRKSCPRG-----YRLIGSSAATCIIISGNTVIMDKKTPVC 153
+ + +G S + Y C G + L+G S C + + V IW P C
Sbjct: 639 TMRNPHGSVVYTRCNPGSGRKFELVGPSPITCTSDPDQGVMSGAPPC 691

Score = 43.0 bits (99), Expect = 0.002
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGTVLANTECRPGY----SGRPSIICLNKSVMTSADCKRKSRRNPDPVNG--MAHYI 110
+G + + + C G+ S + + S+W + + C + NP +NG
Sbjct: 1287 LGAQVDFVCDGRLIGSSAATCIIISGNTVIMDKKTPVCDSELYAFLL 1346

Query: 111 KDIOFGSQRKSCPRG-----KGRILIGSSAATCIIISGNTVIMDKKTPVC 158
DI +G + I Y+C + LIG S+ C GN V W + P C+ +
Sbjct: 1347 GDIPGKELISTCDPDHPRGATNLIGSTIRCTSDPDQGVMSGAPPC 1401

Score = 42.6 bits (98), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTYLANTECRPGYSRRPFS---ITICLNKSVMTSADCKRKSRRNPDPVNG--MA 107
+ +G + NY C G+ S + + S+W + + C + R C PP NG ++ +
Sbjct: 1029 DIOGSRINYSCTGRLIGSSAATCIIISGNTVIMDKKTPVCDSELYAFLL 1088

Query: 108 HVIKDIQFGSQRKSCPRG-----YRLIGSSAATCIIISGNTVIMDKKTPVC 153
+ + +G S + Y C G + L+G S C + + V IW P C
Sbjct: 1089 TMRNPHGSVVYTRCNPGSGRKFELVGPSPITCTSDPDQGVMSGAPPC 1141

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTVLANTECRPGY----SGRPSIICLNKSVMTSADCKRKSRRNPDPVNGMAHYIK 112
+G + + + C G+ S + + S+W + + C + R C PP NG ++ +
Sbjct: 387 LGAQVDFVCDGRLIGSSAATCIIISGNTVIMDKKTPVCDSELYAFLL 445

Query: 113 IQ---FGSQRKSCPRG-----KGRILIGSSAATCIIISGNTVIMDKKTPVC 153
+ + +G + Y+C + LIG S+ C GN V W + P C
Sbjct: 446 LEVFPFGKAVNYTCDPDHPRGATNLIGSTIRCTSDPDQGVMSGAPPC 496

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTVLANTECRPGY----SGRPSIICLNKSVMTSADCKRKSRRNPDPVNGMAHYIK 112
+G + + + C G+ S + + S+W + + C + R C PP NG ++ +
Sbjct: 837 LGAQVDFVCDGRLIGSSAATCIIISGNTVIMDKKTPVCDSELYAFLL 895

Query: 113 IQ---FGSQRKSCPRG-----KGRILIGSSAATCIIISGNTVIMDKKTPVC 153
+ + +G + Y+C + LIG S+ C GN V W + P C
Sbjct: 896 LEVFPFGKAVNYTCDPDHPRGATNLIGSTIRCTSDPDQGVMSGAPPC 946

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPBMLPFPARPTNLTDPF-----EPIGTYLANTECRPGYSRRPFS---ITICLNK-- 81
+P LP PR DP F G+ + Y C PG GR SI C N
Sbjct: 623 IPCGLP---PTIANGDFISTMRNPHGSVVYTRCNPGSGRKFELVGPSPITCTSDND 679

Query: 82 --SWTSADCKRKSRRNPDPVNGMAHYIKD---IQFGSQRKSCPRGRLIGSSA 135
+ + +G + Y+C + LIG S+ C GN V W + P C
Sbjct: 680 QVGWISGAPPCIIIPKCTPPNENGI--LVSDNRSLFSLNEVVEFPCPGVKKGRPV 737

Query: 136 TCIIISGNTVIMDKKTPVC 153
C W+ + P C
Sbjct: 738 KCOALNK---WEPELPSC 752

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPBMLPFPARPTNLTDPF-----EPIGTYLANTECRPGYSRRPFS---ITICLNK-- 81
+P LP PR DP F G+ + Y C PG GR SI C N
Sbjct: 173 IPCGLP---PTIANGDFISTMRNPHGSVVYTRCNPGSGRKFELVGPSPITCTSDND 229

Query: 82 --SWTSADCKRKSRRNPDPVNGMAHYIKD---IQFGSQRKSCPRGRLIGSSA 135
+ + +G + Y+C + LIG S+ C GN V W + P C
Sbjct: 230 QVGWISGAPPCIIIPKCTPPNENGI--LVSDNRSLFSLNEVVEFPCPGVKKGRPV 287

Query: 136 TCIIISGNTVIMDKKTPVC 153
C W+ + P C
Sbjct: 288 KCOALNK---WEPELPSC 302

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPIGTYLANTECRPGYS--GRPSIICLNKSVMTSADCKRKSRRNPDPVNG--MAHYI 110
+P LP PR DP F G+ + Y C PG GR SI C N
Sbjct: 1801 DIPYKELISACDHPDRGNTVNLIGSSAATCIIISGNTVIMDKKTPVCDSELYAFLL 1860

Query: 100 PDPNMGK---AHVTKDIQFGSQRKSCPRGYRLIGSSAATCIIISGNTVIMDKKTPVC 153
P NG HV + G I Y+C GY L+G C G IW C
Sbjct: 1861 KPIQNGHITGCHVSLYLP--GNTISTYCDPDGRLVKGIFICTDQG---TWSQDHYC 1913

Score = 36.7 bits (83), Expect = 0.12
Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PPNLTDPF-----EPIGTYLANTECRPGYSRRPFS---ITICLNK---SWTSADCK 88
P DP F G+ + Y+C GY L+G C G IW C
Sbjct: 1532 PTIANGDFISTMRNPHGSVVYTRCNPGSGRKFELVGPSPITCTSDND 1591

Query: 89 DKCRKSCRRNPDPVNGMAHYIKDIQFGSQ---IKYSGRRLIGSSAATCIIISGNTV 145
+C + P+ N + V + P S I+ C G+ +G S + C +G

Sbjct: 1592 PRGSTMTCACAEVWNL-RVPSNLSFSLTEIRRPGQPGFVWVSHVQQQGNR---1647
 Query: 146 WDKETPYC 153
 W K P C
 Sbjct: 1648 WQPKLPHC 1655

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

```

Query: 35  C NVEEMLPAPRPMTLTDDEFPICGYLYNCRPGYS-GRPFSIT-----CLK-----NSV 83
           C P +P R T + FP G +NY C P G F +I C N V
Sbjct: 430 CPSPFVILPGRHTGKPLEV-FPFGAVNYCDPHPRDGTSPDLLIGESTIRCTSDPGNGV 48

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Query: 84 WTSAKDKCF-RKSCRNPDPVNGMAH---IKIQFGQIKYSCPKGRLLIGSSANCI 139
W+S +C C+P + D G+ +KY C Y S TC+
Sbjct: 489 WSSAPRCILGHQAPDHFLPAKLKTQNNASDPPIGSLKVCRAPEY-YGRPFSITCL- 546

Query: 140 SGNVTIWDNKTPTVC 153
+ ++W + VC
Sbjct: 547 --DNLVWSSPKDVC 558

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPAPRTNLTDPEPPIGYLTANERPGS-GRPSSI-----CLK-----NSV 83
C P +P R T +FP G +NY C P G F +I C N V
Sbjct: 880 CSPPVIENGRIHGTGKPLEV-PPFGKAVNYTCDPHPDGSGTSDLLIGESTIRCTSDPDQNGNV 938

Query: 84 WISAKDKCK-RKSCRNPDPVNGMAIV---IKDIQFGSQIHKYSCRGKRYLLIGSSATGII 139
W+S +C C+ P + D G+ +KY C Y S TC+
WSSDPAPRCGLIHCQADPHFLFAKLQTQNASDPFGISLKYECRPEY-YGRPSTICL- 996
Sbjct: 939

```
Query: 140  SGNVTIWDNKTPEVC 153
          + ++W + VC
Sbjct: 997  --DNLVWSSPKDVC 1008
```

>GSEQ:ARR28562 CRI-4 (116K) analogue.
Length = 543

Score = 253 bits (639), Expect = 7e-67
Identities = 111/121 (91%), Positives = 116/121 (95%)

```

Query: 34 QCNVPEMLPFARPTNLTDDPEEPPIGYTLANYECRPGVSGRPSSIICLNKSVWTSAKDCKR 93
QCN PEMLPFARPTNLTDD+PEEPPIGYTLANYECRPGVSGRPSSIICLNKSVWT AKD-C+R
Sbjct: 1 QCNAPEMLPFARPTNLTDEPEEPPIGYTLANYECRPGVSGRPSSIICLNKSVWTSAGAKDRCR 60

```

Query: 94 KSCRNPDPVNGMAHVITKDIQFGSQIKYSCPKGYRLIGSSATCIIISGTVIMDNKTPVC 153
KSCRNPDPVNGM HVIK IQFGSQIKYSC KGYRLIGSSATCIIISG-TVIMDNKTPVC
Sbjct: 61 KSCRNPDPVNGMAHVITKGIQFGSQIKYSCTKGYRLIGSSATCIIISGTVIMDNKTPIC 120

Query: 154 D 154
D
Sbjct: 121 D 121

Score = 128 bits (319), Expect = 2e-29
Identities = 58/92 (63%), Positives = 65/92 (70%)

Query: 35 CNPPEWLPPARPTNLTDEEFPICGYLNECRPGYGRPFSTICLKNSVMTSAKDCKRK 94
C P+ PA+ T+ +PPIGT L YECRP Y GRPFSI CL N VM+S KD CKRK
Sbjct: 452 COAPDHPLPAKLKYTNASIPFGISLKECRPEYVGRPFSITCLDNLVMSPRDVCARK 511

Query: 95 SCRNPEDVNGMAHVIKDIQFGSQIKYSCFXG 126
SC+ PEDPVNGM HVI DIQ GS+I YSC G
Subject: 512 SCRTPEVNGMVHVTIDQVGRINYSCTTG 543

Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFFDQCINPFWLBPAPRNLTDDFFPIGTIANYECKPGYSR-PFSIICLKSNVWS 86
L S S C P + A T D F G + Y C PGY R S + C W+
Sbjct: 249 LPSGRVCCPPEDVLHAERQGRKD-NFSPGQEVYFSCPGYDLGGAAMRCPTQGMSP 307

Query: 87 AKDKCKRKSCRN-PPDPVANCMAHYIKIDIFGSGQTKYSCCKGYRLIGSSATCIIISGNVI 145
A C+ KSC + +NG ++G+++ + C +G+L GSS++ C+++ +
Sbjct: 308 AAPCEVKSQCDPMQQLNQRVLFPVNLQGAKVDFVCEGFGQLKGSASVYCVLAGMEST 367

Query: 146 WDNKTPVCD 154
W++ PVC+
Sbjct: 368 WNSSVPVCE 376

Score = 43.8 bits (101), Expect = 9e-04
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTYLNVECRDPY-----SGRPSTICLKNWVTSAKDKCKRKSCHRNPPDPVNG--MAHYK 111
G+ + Y C GY S II +W + C R C Pp NG ++ +
Sbjct: 83 GSQIKSCTMGYRLGSSSNTCISGDIYIMDNKTPICDRIPCGLPPTINGDFISTNRE 142

Query: 112 DIOFGSQIKVSCPXG-----YRLIGSSSATCIISGNV-IWDNKTPEVC 153
 + +GS + Y C G + L+G S C + + V IW P C
 Sbjct: 143 NPHVGSVVTYRCHPBGSGGRKVFELVGEPSICTSNDQVGLMSGPAPQC 191

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

```

Query: 57  IGYLVNVECRPGY-----SGRPFSIIICLKNVMTAKDKCKRKSCKRNPDVPVNGMAHTVD 112
          +G  +++ C  G+   S   ++   S+W S+   C++  C  +pp  NG  H  K
Sbjct: 337 LGAKVDFVCEBGFQOLKGSSASYCVLAGMELMNSSVPVCEQIFCPSPVPIPNG-RHTGKP 395

```

```

Query: 113 IQ---FSGIKYSCP-----KGYRLIGSSATCII--SGNTVIMDKNTPVC 153
      ++   FG + Y+C           + LIG S+ C      GN V W + P C
Subject: 396 LEVTFPGKAVNTCDPHPRGTSFDLIGESTIRCTSDPQNGV--SSPAPRC 446

```

Score = 34.0 bits (76), Expect = 0.76
Identities = 32/138 (23%), Positives = 50/138 (36%), Gaps = 29/138 (21%)

```

Query: 37  VEWMLPAPRTNLTDDP-----EPDICTVLNVECKPGVSGRPF-----SIICLKN-- 81
           +P LP PT DP F G+ + Y C PG GR SI C N
Sbjct: 123 IPCGLP--PITNGDFISTNRENFHYGSAVTTYRCNPGSGGRKVELVGEPSIYCTSNDD 17

```

```

Query: 82  --SWTSAKDCKRKRSCRNPPDPVNGMAHYIKD-----IQFSQIKVSCPKGYRLIGSSA 135
          +W+  +C  +  PP  NG+  ++ D          +++ C  +  + G
Subject: 180 OVGWISGPAQCIIIPNKCDDPNVENGI--LVSDNRSLFSLNEVEVERCQPVVPMKGPRRV 237

```

Query: 136 TCISGNTVIMDNKTPVC 153
C W+ + P C
Subject: 238 KCOALNK---WEPELPSC 252

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNUPEMLFPARPNTLTDDEFPIGTIYINCYCRGYS-GRPSII-----CLK-----NSV 83

Query: 360 CSEPVITNGHHTGKPLEV--FPFGKAVNYTDDPHDRGTSFDLIGSTIRCTSDPQNGV 438
+G S C P + P G +NY C P G F +I C N V
Sbjct: 360 CSEPVITNGHHTGKPLEV--FPFGKAVNYTDDPHDRGTSFDLIGSTIRCTSDPQNGV 438

Query: 84 WTSADCKR-RKSCNRPDPVNGMAHV---IKDIQSGQIKYSCPGYRLIGSSANCI 139
+S +C +C P + D G +KY C Y S TC+
Sbjct: 439 WTSAPRKGILGHCOAIDHPLFAKLTQYMASDPPIGTSLKREPRY-VGRPFSTICL- 496

Query: 140 SGNVTYMDNKPVC 153
+ +W + VC
Sbjct: 497 --DNLMWSSPDVC 508

>GSEQ:IAAB28552 CRI-4 (78T, 79D) analogue.
Length = 563

Score = 252 bits (636), Expect = 2e-66
Identities = 110/121 (90%), Positives = 116/121 (94%)

Query: 34 QCNVEMLPAPAPNLTDDEPPIGTIYANECRPGYSGRPFSTICLNKSWTSADCKR 93
QCNVEMLPAPAPNLTDDEPPIGTIYANECRPGYSGRPFSTICLNKSWT AKD+C+R
Sbjct: 1 QCNVEMLPAPAPNLTDDEPPIGTIYANECRPGYSGRPFSTICLNKSWTAKDCRR 60

Query: 94 KSCNRPDPVNGMAHVIKDIQSGQIKYSCPGYRLIGSSANCIISGNVTYMDNKPVC 153
KSCNRPDPVNGMAHVIKDIQSGQIKYSCPGYRLIGSSANCIISGNVTYMDNKPVC
Sbjct: 61 KSCNRPDPVNGMAHVIKDIQSGQIKYSCPGYRLIGSSANCIISGNVTYMDNKPVC 120

Query: 154 D 154
D
Sbjct: 121 D 121

Score = 128 bits (319), Expect = 2e-29
Identities = 58/92 (63%), Positives = 65/92 (70%)

Query: 35 CNVEMLPAPAPNLTDDEPPIGTIYANECRPGYSGRPFSTICLNKSWTSADCKR 94
C P +P R T + +PPIGT L YECR P G + Y C PGY R S+ C R
Sbjct: 452 CQAPDHPLFAKLTQYMASDPPIGTSLKREPRYGRPFSTICLNKSWTSADCKR 511

Query: 95 KSCNRPDPVNGMAHVIKDIQSGQIKYSCPG 126
SC+ PDPVNGM HVI DIQ GS+I YSC G
Sbjct: 512 SCRTPEPDPVNGMAHVITDIQVGRINYSCTTG 543

Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFSQCNVPEMLPAPAPNLTDDEPPIGTIYANECRPGYSGRPFSTICLNKSWTS 86
L S S C P + A T D P G + Y C PGY R S+ C R W+
Sbjct: 249 LPSCSNVQPPPVLAERQKDK-NFSRQGVETSCERPDRLQASMKCTPGQMSR 307

Query: 87 AKKCKRSCRN-PDPVNGMAHVIKDIQSGQIKYSCPGYRLIGSSANCIISGNVTI 145
A C K RSC + +NG +Q G+++ + C +G+TL GSS+ C+G+
Sbjct: 308 AATPCVSCDQWGLNGVLPVNIQAKVDCDPSQLGSSASTCVLAWESL 367

Query: 146 WDKTTPVCD 154
W+ + PVC+
Sbjct: 368 WNSVPCVCE 376

Score = 44.1 bits (102), Expect = 7e-04
Identities = 30/113 (26%), Positives = 45/113 (39%), Gaps = 13/113 (11%)

Query: 54 EPIPIGTANTCEKPGY----SGRPFSTICLNKSWTSADCKRSCNRPDPVNG--MA 107
+ G + Y C GY S II +W + C R C PP NG ++
Sbjct: 79 DIQSGQIKYSCPGYRLIGSSANCIISGNVTYMDNKPVCIRLPGCLPTITMDRTIS 138

Query: 108 HVIKDIQSGQIKYSCPGY----YALIGSSANCIISGNVTI-MDNKTPVC 153
++ +G S C G +L+G S C + + V IM P C
Sbjct: 139 TURENFHYGSVVYACNPGSGGRKVFELVGEPSICTSDQVIGWGPAPQC 191

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTANTCEKPGY----SGRPFSTICLNKSWTSADCKRSCNRPDPVNGMAHVIK 112
+G +++ C G+ S + + + S+W S+ C+P NG H R
Sbjct: 337 LQAKVDCDPSQLGSSASTCVLAGESWNSVPCQIPCSPPVPLNG-RHNGR 395

Query: 113 IQ--FGQIKYSCP-----KGRILIGSSANCI--SGNVTYMDNKPVC 153
++ +P G + + + C +LIG S+ C GN V W + P C
Sbjct: 396 LEVPPFGKAVNYTDDPHDRGTSFDLIGSTIRCTSDPQNGV-WSSPAPRC 446

Score = 34.0 bits (76), Expect = 0.76
Identities = 32/138 (23%), Positives = 50/138 (36%), Gaps = 29/138 (21%)

Query: 37 VEMLPAPAPNLTDDEPPIGTIYANECRPGYSGRPF-----SILCLAK-- 81
+P LP PT DF P G+ + Y C PG GR SI C N
Sbjct: 123 ITCGLP---PLTNGDPISTNRENFHYGSVVYACNPGSGGRKVFELVGEPSICTSDND 179

Query: 82 --SWTSADCKRSCNRPDPVNGMAHVIKD---IQSGQIKYSCPGYRLIGSSA 135
+W +C + PP+ NG+ ++ D + + + C + + G
Sbjct: 180 QVIGWGPAPQCIIIPNCTPWNENG--LVSDNLSLPLNVEVFPNCQVYVMGRRV 237

Query: 136 TCIISGNVTYMDNKPVC 153
C
Sbjct: 238 KQALAK--WPELPSC 252

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVEMLPAPAPNLTDDEPPIGTIYANECRPGYSGRPFSTICLNKSWTSADCKR 94
C P +P R T + P P G +NY C P G F +I C N V
Sbjct: 380 CSEPVITNGHHTGKPLEV--FPFGKAVNYTDDPHDRGTSFDLIGSTIRCTSDPQNGV 438

Query: 84 WTSADCKR-RKSCNRPDPVNGMAHV---IKDIQSGQIKYSCPGYRLIGSSANCI 139
W+S +C C+ P + D G +KY C Y S TC+
Sbjct: 439 WTSAPRKGILGHCOAIDHPLFAKLTQYMASDPPIGTSLKREPRY-VGRPFSTICL- 496

Query: 140 SGNVTYMDNKPVC 153
+ +W + VC
Sbjct: 497 --DNLMWSSPDVC 508

>GSEQ:IAAB26823 Membrane targeted complement inhibitor peptide.
Length = 198

Score = 251 bits (635), Expect = 2e-66
Identities = 110/121 (90%), Positives = 116/121 (94%)

Query: 34 QCNVEMLPAPAPNLTDDEPPIGTIYANECRPGYSGRPFSTICLNKSWTSADCKR 93
QCNVEMLPAPAPNLTDDEPPIGTIYANECRPGYSGRPFSTICLNKSWT AKD+C+R
Sbjct: 2 QCNVEMLPAPAPNLTDDEPPIGTIYANECRPGYSGRPFSTICLNKSWTAKDCRR 61

Query: 94 KSCNRPDPVNGMAHVIKDIQSGQIKYSCPGYRLIGSSANCIISGNVTYMDNKPVC 153
KSCNRPDPVNGMAHVIKDIQSGQIKYSCPGYRLIGSSANCIISGNVTYMDNKPVC
Sbjct: 62 KSCNRPDPVNGMAHVIKDIQSGQIKYSCPGYRLIGSSANCIISGNVTYMDNKPVC 121

Query: 154 D 154

D
Sbjct: 122 D 122

Score = 43.8 bits (101), Expect = 9e-04
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GYLYNTECRPGY---SGRPSTICLNKSWTSADCKKSCRNPPDPVNG--MAHYIK 111
G+ + Y C GR S II +W+ C R C R P NG + + +
Sbjct: 84 GSQIKYSCYGRLLIGSSATYCIISGDTVMDEPPICDHPCGLPTINMGFISTNRE 143
Query: 112 DIQFGSQIKYSCPKG-----YRLIGSSATYCIISGNTV-INDNKTPTVC 153
+ +GS+ Y C G +L+G S C + + V IW P C
Sbjct: 144 NPHYSVVTYRCNPGSGRKVFELVGEPSYICTSNDQVIGMSGAPQC 192

>GSEQ:AA26817 Membrane targeted complement inhibitor peptide.
Length = 198

Score = 251 bits (635), Expect = 2e-66
Identities = 110/121 (90%), Positives = 116/121 (94%)

Query: 34 OCNVPEMLPPARPPTLMDPEPIGTLYNTECRPGSGRPSTICLNKSWTSADCKK 93
OCN PEMLPPARPPTLMDPEPIGTLYNTECRPGSGRPSTICLNKSWT AED-C+R
Sbjct: 2 OCNAPEMLPPARPPTLMDPEPIGTLYNTECRPGSGRPSTICLNKSWTQADNCR 61
Query: 94 KSCRNPPDPVNGMAHYIKDIQFGSQIKYSCPKGRLIGSSATYCIISGNTVINDNKPVC 153
KSCRNPPDPVNG MAHY IQFGSQIKYSC KQRLIGSSATYCIISG+FYIND+TF+C
Sbjct: 62 KSCRNPPDPVNGMAHYIKDIQFGSQIKYSCYGRLLIGSSATYCIISGDTVMDEPPICT 121
Query: 154 D 154
Sbjct: 122 D 122

Score = 43.8 bits (101), Expect = 9e-04
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GYLYNTECRPGY---SGRPSTICLNKSWTSADCKKSCRNPPDPVNG--MAHYIK 111
G+ + Y C GR S II +W+ C R C R P NG + + +
Sbjct: 84 GSQIKYSCYGRLLIGSSATYCIISGDTVMDEPPICDHPCGLPTINMGFISTNRE 143
Query: 112 DIQFGSQIKYSCPKG-----YRLIGSSATYCIISGNTV-INDNKTPTVC 153
+ +GS+ Y C G +L+G S C + + V IW P C
Sbjct: 144 NPHYSVVTYRCNPGSGRKVFELVGEPSYICTSNDQVIGMSGAPQC 192

Database: Current.Geneseq.AA.fasta
Posted date: Apr 14, 2003 12:19 PM
Number of letters in database: 150,621,602
Number of sequences in database: 1,029,157

Lambda K 0.323 H 0.456

Gapped
Lambda K 0.270 H 0.230

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to Db: 62790668
Number of Sequences: 1029157
Number of Extensions: 2617728

Number of successful extensions: 10088
Number of sequences better than 10.0: 685
Number of HSP's better than 10.0 without gapping: 286
Number of HSP's successfully gapped in prelim test: 399
Number of HSP's that attempted gapping in prelim test: 6318
Number of HSP's gapped (non-prelim): 2814
length of query: 174
length of database: 150,621,602
effective HSP length: 46
effective length of query: 128
effective length of database: 103,280,380
effective search space: 1321988640
effective search space used: 1321988640
T: 11
A: 40
X1: 16 (7.5 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 41 (21.9 bits)

Graphical View...

Submit sequences to: BLAST2

Submit

Reset



Cluster Results

Retrieval	BLAST2	FASTA	ClustalW	CCG Assembly	Phrap	Translation
-----------	--------	-------	----------	--------------	-------	-------------

☐ GSEQ:AAZ38150
☐ 103561CB1

Sequence format is Pearson
Sequence 1: GSEQ_AZ38150 6951 bp
Sequence 2: 103561CB1 627 bp
Start of Pairwise alignments

$$\frac{325}{629} \times 100\% = 51.8\%$$

```
Aligning...
Group 1: Sequences:      2      Score:18429
Alignment Score 3045
CLUSTAL-Alignment file created [ba0Nay0L.aln]
CLUSTAL W (1.7) multiple sequence alignment
```

GSF02_AJ238150
 103561CB1
 -----CGTGGTTTGA-GATGGAGAGGGA
 CGAGATCAAGAGGAGCTTCCCTGCTGGGTTCGCGTTCGCTGCACCTCCGAT

 GATTCGGGACCTCTTCTCCAGAGAGCCGAGACCTCTGAGC--CGCGAGC-CCGGATC
 AATATCAGCGATCTCCCGGCGCGCTCATAGGCGCTCCGCTGCTGTGAGGATCCCTTTC

 TCCTCTTTCGCTGCGGAGGATCCCTGCTGAGCGATGATGATGCTCTGAGCGCTGCGAGTGG
 CTTCGCGAGCTTTCCTGCGGATGCTTCGCGGCGCCCTGGATTTATCT--CGTTCCTCT

 CTTAGGGGATTAATGCAATGCCCCAGAAATGAGCTTCCATTATTCGACGAGCTACCACTTAATG
 TCTGCATATATGCAATGCTGCAATGAGTGTTCATATTCGACGAGCTCTACCACTTAATG

 ATGAGTTTATGATTTCCCATATGAGGACATATCTGAACTATGATGCGCCCTGGATTATTCG
 ATGACTTATAGATTTCCCATATGAGGACATATCTGAACTATGATGATGCGCCCTGGATTATTCG

 GATGACCGTTTTCATCATCTGACCTAAAAAACTCAGCTTGAATCTGCTAAAGGACAGGT
 GATGACCGTTTTCATCATCTGACCTAAAAAACTCAGCTTGAATCTGCTAAAGGACAGGT

57

5/5/03 9:06 PM

[illegible]

10

ClustalW Results		http://patents.incyte.com:8000/cgi-bin/SqServer/SqServer	ClustalW Results	http://patents.incyte.com:8000/cgi-bin/SqServer/SqServer
103561CB1	-----			
GSEB_AA238150 103561CB1	ATTAGCACCAAGAGAGAAATTTTTCACATNGAATCAGTGTGACCTTACCCGTGCATATCTT		GSEB_AA238150 103561CB1	ACCCCAAGAGAGATTTCATTTGCCAGTCCCTACGATCCCAATTAATGACTTTGAGTTTCCA
GSEB_AA238150 103561CB1	GGAAGCAGAGGAGAAAGGTGTTTGAAGCTTGTGGGTGAGCCCTCCATATATCTGCAACAGC		GSEB_AA238150 103561CB1	GTCGGGACATCTTTGAAATTATGAAATGCCGTCTGGGTATTTTGGGAAAAATGTTCTCATATC
GSEB_AA238150 103561CB1	AATGACGATCAAGTGGGCAATCGAGCGGCCCCGCCCTCAGTGCATTTATACCTTAACAA		GSEB_AA238150 103561CB1	TCCTGCTTAGAAAACTTGGTCTGGTCAAGTGTGAAGACACTGTAAAGCAAAATCATGT
GSEB_AA238150 103561CB1	TGCACGCTCCAAATGTGAAATAATGAAATATTGTGATCTGACACAGAACCTTAATTTTTC		GSEB_AA238150 103561CB1	GGACTCCACCAAGAACCTTTCATGGAATGTGTGATATTAACACAGATACACAGTTTGA
GSEB_AA238150 103561CB1	TTAAATGAAGTTGTGAGTTTAAAGTTTAAAGCTGGCTTGTGTCAATGAAGAACCCGCCGT		GSEB_AA238150 103561CB1	TCAACAGTTAATTATCTTGTATATGAAGGGTTTCAGCTCATTTGGTCCCATCTACTACT
GSEB_AA238150 103561CB1	GTGAAGTGCAGGCGCTTGAAACAAATGGAGCCAGATTCACAGCTGCTCAAGGTTGTGT		GSEB_AA238150 103561CB1	TGCTCTGTCTCAGGCAATATATGTCAATAGGAATGAAGGCACTTATTTGTGAGATCATAT
GSEB_AA238150 103561CB1	CAGCCGCTCCAGAAATCCCTCAGTGTGACATACCCCAAGCATCAGACAACTTTTCA		GSEB_AA238150 103561CB1	TCCTTGTGAGCCACCTCAACCATATCCAAATGGAGACTTACAGCAATATTAAGAACATCT
GSEB_AA238150 103561CB1	CTTGGGCAAGAAAGTTTCTTACAGCTGTGAGCCTGGCTATTAACCTCAGAGGGGCTGCCTT		GSEB_AA238150 103561CB1	TTTTCACAAATGGAACGGTGTAACTTATACAGTGGCCACATCGAACAGATGGAACAGCTG
GSEB_AA238150 103561CB1	CTGCATCTGCACACCCAGGAGACTGAGACCTTGAAAGCCCGAAGATGTGCAATGAAATCC		GSEB_AA238150 103561CB1	TTTGAAGTTTGGAGAACGGTCAATATATTGCACACGAAAGATGATCAAGTTGTGTT
GSEB_AA238150 103561CB1	TTGTATGACTTCTTGGGTCAATCTCCCTCATGGCCGTGTGCTATTTTCCACTTAATCTCAG		GSEB_AA238150 103561CB1	TGGAGAGCCCTCCCTCGGTGTATTTTCTACTAATTAATGCAAGCTCAGAAAGTTGAA
GSEB_AA238150 103561CB1	CTTGGGGCAAAAGTGTCTTTGTCTGTGATGAAGGTTTCCTTAAGGGCAATTCGTT		GSEB_AA238150 103561CB1	AATGCCAATTAGAGTACAGGAACAGAGATTTCTTTTCCCTCAGTGAATCAAGATTT
GSEB_AA238150 103561CB1	AGTCAATGTGTCTTGGTTGGAATGGAAGCTTTTGAATTAACATGTGTCTCTGTGTGAA		GSEB_AA238150 103561CB1	AGATGTCAAGCCGGGTTTGTATGTGATGGGTCCCAACTGTGTGAGTCCAGACCAATGGC
GSEB_AA238150 103561CB1	CATATCTTTTGTCCAAATCTCTCAGCTATCTTAATGGAGACACACAGGAATCTCCCTCT		GSEB_AA238150 103561CB1	AGATGGGGGGCCCAAGCTGCACTGTCTTCAGAGGTGTGTGAGCCGCTCCAGAAATCTCTG
GSEB_AA238150 103561CB1	GAGATATATTCCCTTATGAAAAAATAATCTTAACAATGTGACCCCAACCAAGACAGAGGG		GSEB_AA238150 103561CB1	CATGTGAGCATATACCTTAAGCAATCAGAGCAACTTTTCACTTGGGCAAGAAATGTCTTAC
GSEB_AA238150 103561CB1	ATGACCTTCAACTCATTTGGGAGAGACCATCCGTGACAAAGTGAACCTCATGGGAAT		GSEB_AA238150 103561CB1	AGCTGTAGCCCAAGCTAATGACCTTCAGAGAGGGGCTGCTGTGTGCACTGTCAAGCCCAAGGA
GSEB_AA238150 103561CB1	GGGGTTTGGAGACAGCCCTGCTTCGCTGTGAATCTTTGTGTCTGTGCTGTGATCACTGTAA		GSEB_AA238150 103561CB1	GACTGAGCCCTTGAGAGCCCTTAAGATGTACATGTAAATCTCTGTGATGACTTCTTGGGCCAA

ID	AA238150	
CS	14867ac5163e7e04c7b1d831b469abbl	
IDH	AA238150 standard; DNA; 6951 BP.	
MO	DNA	
DV	20-MAR-2003 (updated)	
DT1	22-FEB-2000 (first entry)	
DT2	22-FEB-2000	
DT	PATENT US5981481-A	
AK	PRIMARY AC	AA238150
EAK		
DR	P-PSDB MAY55751	
DR	WPI 1999-633357/54	
EDR		
DE	Human C3b/C4b receptor (CRI) protein encoding DNA.	
KW	Arthus reaction	
KW	C3b/C4b receptor	
KW	CRI protein	
KW	autoimmune disorder	
KW	cell-surface protein	
KW	complement pathway enzyme	
KW	complement regulatory activity	
KW	diagnostic	
KW	erythrocyte	
KW	heart condition	
KW	human	
KW	inflammation	
KW	myocardial infarct	
KW	reperfusion injury	
KW	ss	
KW	tissue damage	
KW		
EXW	Homo sapiens	
OS	4a22b91c1bf65eca55a089eb4312eae	
SC	HOMO SAPIENS	
SP		
ESP		
INST	(AAVAN-) AVANT IMMUNOTHERAPEUTICS INC	
CC	The invention relates to a human C3b/C4b receptor (CRI) protein. The CRI	
CC	protein or fragment is expressed as a cell-surface protein on the surface	
CC	of a non-human cell and exhibits a complement regulatory activity of full	
CC	length human CRI as expressed on erythrocytes. The CRI function in vivo	
CC	may be mediated through the inhibition of complement pathway enzymes. The	
CC	soluble CRI protein exhibits a complement regulatory activity, and this	
CC	may be used to prevent reperfusion injury, inhibit Arthus reaction, and	
CC	neutrophil mediated tissue damage, and reduce myocardial infarct size,	
CC	and inflammation. The CRI protein and its fragments can also be used in	
CC	the treatment of conditions which involve unwanted complement activity,	
CC	e.g. shock lung, tissue damage due to burn, or ischemic heart conditions,	
CC	and autoimmune disorders. CRI proteins, analogues, derivatives, and anti	
CC	-CRI antibodies are used in assays, and diagnostics. The present sequence	
CC	represents a DNA encoding the human CRI protein.	
CC	(Updated on 20-MAR-2003 to correct PR field.)	
CC		
EC	fe0184ae97550db68750baf74d037fed	
RN	PD: 09-NOV-1999. PF: 06-JUN-1995; 95US-0470652. PR: 03-APR-1989; 89US-0332865.	
RC	24-FEB-1993; 93US-0026134. PR: 06-DEC-1994; 94US-0350238. PR: 01-APR-1988; 88US	
RT	A human C3b/C4b receptor (CRI) protein having antiinflammatory and cardiant ac	
RL	Patent: US5981481-A. Disclosure; Fig 1A-P; 87dp; English.	
RA	Concino M. F.	CONCINO MF
RA	Mong W. W.	WONG WM
RA	Makrides S. C.	MAKRIDES SC
RA	Klickstein L. B.	KLICKSTEIN LB
RA	Peaton D. T.	PEATON DT
RA	Ip S. H.	IP SH
RA	Marsh H. C.	MARSH HC

[illegible]

BLAST2 Search Results

biology in situ

die

SLA:

BLAST2 Manual

SeqServer Version 4.8 Jan 2002

Current.Geneseq.NA.fasta



Schschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Zheng Zhang, Webb Miller, and David J. Lipman (1997), 'and PSI-BLAST: a new generation of protein database search cteic Acids Res. 25:3389-3402.

**B1
letters)**

ent.Geneseq.NA.fasta.
61,325 sequences; 1,289,285,926 total letters

.....done

Inducing significant alignments:

602	Human RECAP polymucleotide, SEQ ID NO: 30.	1243	0.0
603	Human coding sequence SEQ ID 39.	1229	0.0
604	DNA encoding novel human diagnostic protein #94	682	0.0
605	Human mdct cDNA SEQ ID 247.	599	e-169
606	Human C3B/C4B receptor CRI (complement receptor	599	e-169
607	Human cDNA differentially expressed in granuloc	599	e-169
608	Human polymucleotide SEQ ID NO 583.	599	e-169
609	Human C3b/C4b receptor (CRI) protein encoding D	599	e-169
610	Entire human complement type 1 receptor coding	599	e-169
611	CRI protein DNA.	599	e-169

2 Human RECAP polynucleotide, SEQ ID NO: 30.

length = 627

bits (627), Expect = 0.0

627/627 (100%)

s / Plus

5/5/03 8:27 PM

Sbjct: 39
 cgagactcgaagggagacatccctctgcctcggctgcctcttcctcgttctctctgcctacactccgag 98

```
Query: 61 aaatcaagggtcttcacgcgacctcagccgatcgacttccc 120  
|||  
|||||  
Sbjct: 99 aaatcacgggtctcccgaccgcatatgcccccccgctcctcgaagtcccttc 158
```

Query: 121 cctcccgcgcttccctgggttgcttcctggcgaccttgatgctgctcctctt 180
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 159 cttcccgagcttccctgggttgcttcggcgacccctgatgctgctcctctt 218

Query: 181 ccgacccaatgccaatgtcccggaatgcttcacatctggccaagcccaaccaactaacgatg 240
|||||
Sbjct: 219 ccgacccaatgccaatgtcccggaatgcttcacatctggccaagcccaaccaactaacgatg 278

Query: 241 accttgagttcccatctggacatactgaactgaatgcccgcctfgtcatccgaa 300
 |||||
 Sbjc: 279 accttgagttcccatctggacatactgaactgaatgcccgcctfgtcatccgaa 338

Query: 301 gaccgctttctcatcatctgcctaaaaaactcagctcttgacaaagtctaaagacaaagtgc 360
 |||||
 Sbjct: 339 gaccgctttctcatcatctgcctaaaaaactcagctcttgacaaagtctaaagacaaagtgc 398

Query: 361 aacgtaaatcatgtctgtaatccctccagatccctgtgaatgcatgacatgtgacaaag 420
 |||||
 Sbjct: 399 aacgtaaatcatgtctgtaatccctccagatccctgtgaatgcatgacatgtgacaaag 458

Query: 421 acatccagttccgatacccaataaattcttgcctcaagatacgaactatggtc 480
 |||||
 Sbjct: 459 acatccagttccgatacccaataaattcttgcctcaagatacgaactatggtc 518

[illegible]

Query: 541 ttctgtaacagtgaattggaatgatcatctccattctcttcacgatacatcttaatttc 600
|||||
Sbjct: 579 ttgtgtacagtgagcttggaatatgatctctattctcttttaccgatacatcttaatttc 638

```
Query: 601 ctctggaataataaaatct 620
      |||||
Sbjct: 639 ctctggaataataaaatct 658
```

>GSEQ:AAS64290 DNA encoding novel human diagnostic protein #94.
Length = 9038

```
Score = 682 bits (344), Expect = 0.0
Identities = 546/580 (94%), Gaps = 30/580 (5%)
Strand = Plus / Plus
```

Query: 1
cgagactcgaaggagacattccctgcctcgcgtgctcttcgctctctcgtcctcaactccgag 60
|||||
Sbjc: 1583
cgagactcgaaggagacattccctgcctcgcgtgctcttcgctctctcgtcctcaactccgag 1622
|||||

Query: 61
aaatcagcggtctcccgccgcctcatgctgcctcccgctccgctctcagagctccc-ttc 119

Objct: 1643 aaatcacgggtctctccgcgcgcgtcatgagcgtctccgcgtctctcgagcgtcccttc 1702

Query: 120 ccttcccgagcttctcct-gggtcacttcgagcgccct-gtgtgtgctgctgtctcctcct 177

Subjct: 1703 cctcccgccgcttccctcggggtctgtcctctcgcgcgcacctcgggtgtgtcgtcgtcgtcctcct 1762

Query: 178
tctccgatcaat-gcaatgtcccgaaat-ggcttcca-tttgcaa--ggcctacc-aacc 231

Subjct: 1763 tctcgcgatcgaatgcatgtcccggaatggtcttccaatttgtccaggtgtcttaccaaac 1822

Query: 232 taactgatgactcttgagttcccat-gggacatat-cbgaactatgaaagcc--ggcct 287

Sbjct: 1823 taactgatgaattcgaagtttcccatgtgggacatattcctgaactatgaatgccgcgcccc 1882

Query: 288 ggttatc-ccggaagaccgtttc-ctatcatctg-cttaaaaaaactcagrtc-ggacaag 343

Sbjc: 1883 ggtatctccggaagaccgcttctctatcatctgcctaaanaactcagctcgggacaag 1942

Query: 344 tgcgaagacaagtcgcaacg-taatcatg-tcgtaatc-tccagatcctgtgaat-q 399

Subject: 1943 tgcctaaggacaagltgcaaacgttaataatcatcgttcgtaatccctccagatcccggtgatgg 2002

Query: 400 gcatggcacatgtg--atcaagacatccag-ttcgga-tcccaa-ttaatatctta 454

Sbjct: 2003 gcatggacatgtgattcaagaacaccagtttcgattcccaaatcaatatcttg 2062

Query: 455
-tcctaagagataccgcactcattgg--ttcctcgtctcaccacat-gcatcatctcaacca 510

Sbjct: 2063 ttcttaagataccgactcatgtttctctcgctgcacacatgcacatctcagca 2122

Query: 511 acactgtcatttggataataaaacaccctatttcacaa 550

Sbjct: 2123 acacgctcattcgggataataaacacactgttttqtgacag 2162

Score = 97.6 bits (49) . Expect = 3e-18

identities = 130/151 (82%)
Strand = plus / plus

Query: 360 aaacbaaatcatatcataatcctccagatcctcttgaatnccatnccaatatncaaa 410

Sbjct: 4672 aaacgtaaatcatgttaaaccctccagatccagtggaatgcacatgcatgcatgcaca 4731

Query: 420 gacatccacttcgagatcccaaataaatattcttttctctaaacgatacccgaaatcaatttctt 470

Sbjct: 4732 gacatccaggttgatccagaatcaactatcttqtaacaggaacacccaatcatttgt 4791

Query: 480 factctctcttcacatatccatctatctcaccaccccactn 516

Subjct: 4792 cactcatctgctgaatgatctctcagaacaaatctc 4828

Score = 95.6 bits (48), Expect = 1e-17
Identities = 102/120 (85%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcgtcgttaatccctccagatccctggaatgcatgagcatgcatgaca 419
|||||
Sbjct: 3322 aaacgtaaatcgtcgttaatccctccagatccctggaatgcatgagcatgcatgaca 3381

Query: 420 gacatccaggttcggatcccaaatatattctgtcctaaggataccgcatctggt 479
|||||
Sbjct: 3382 gacatccaggttcggatcccaaatatattctgtcctaaggataccgcatctggt 3441

Score = 61.9 bits (31), Expect = 2e-07
Identities = 73/87 (83%)
Strand = Plus / Plus

Query: 208 ttccatttgcaggcccttaacccaactgaacttgaatttccattggagcatatc 267
|||||
Sbjct: 5879 ttccatttgcaggcccttaacccaactgaacttgaatttccattggagcatatc 5938

Query: 268 tgaactatgaatgcgcgccttggtatt 294
|||||
Sbjct: 5939 tgaactatgaatgcgcgccttggtatt 5965

>GSEQ.ABX34686 Human mdlt cDNA SEQ ID 247.
Length = 7385

Score = 599 bits (302), Expect = e-169
Identities = 350/366 (95%)
Strand = Plus / Plus

Query: 185 tcaatgcaatgctccggaatggtcttccattgcccaggccttaacccaactgaatgatt 244
|||||
Sbjct: 153 tcaatgcaatgctccggaatggtcttccattgcccaggccttaacccaactgaatgatt 212

Query: 245 tgaatttcccatgggacatatctgaactatgaatgacgcgccttggtattccggagacc 304
|||||
Sbjct: 213 tgaatttcccatgggacatatctgaactatgaatgacgcgccttggtattccggagacc 272

Query: 305 gtttttcatcatctgcttaaaaaaacctcagcttggacaaagtgttaagacaaagtgcagaacg 364
|||||
Sbjct: 273 gtttttcatcatctgcttaaaaaaacctcagcttggacaaagtgtgtcagaacg 332

Query: 365 taaatcatgctgaatcctccagatccctggaatgcatgagcatgcatgacaagaatc 424
|||||
Sbjct: 333 taaatcatgctgaatcctccagatccctggaatgcatgagcatgcatgacaagaatc 392

Query: 425 ccaggttcgagatcccaatataatctgttcctaaggataccgactcattggtcttc 484
|||||
Sbjct: 393 ccaggttcgagatcccaatataatctgttcctaaggataccgactcattggtcttc 452

Query: 485 gtcctgcacatgcatcatcctcaggcaaacctgcatcttggagataataaaacacctgttg 544
|||||
Sbjct: 453 gtcctgcacatgcatcatcctcaggcaaacctgcatcttggagataataaaacacctgttg 512

Query: 545 tgcagc 550
|||||
Sbjct: 513 tgcagc 518

Score = 97.6 bits (49), Expect = 3e-18
Identities = 130/157 (82%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcgtcgttaatccctccagatccctggaatgcatgagcatgcatgaca 419
|||||
Sbjct: 3028 aaacgtaaatcgtcgttaatccctccagatccctggaatgcatgagcatgcatgaca 3087

Query: 420 gacatccaggttcggatcccaaatatattctgtcctaaggataccgcatctggt 479
|||||
Sbjct: 3088 gacatccaggttcggatcccaaatatattctgtcctaaggataccgcatctggt 3147

Query: 480 tccctgctcgcacatgcatcatcctcaggcaaacctg 516
|||||
Sbjct: 3148 tccctgctcgcacatgcatcatcctcaggcaaacctg 3184

Score = 95.6 bits (48), Expect = 1e-17
Identities = 102/120 (85%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcgtcgttaatccctccagatccctggaatgcatgagcatgcatgaca 419
|||||
Sbjct: 1678 aaacgtaaatcgtcgttaatccctccagatccctggaatgcatgagcatgcatgaca 1737

Query: 420 gacatccaggttcggatcccaaatatattctgtcctaaggataccgcatctggt 479
|||||
Sbjct: 1738 gacatccaggttcggatcccaaatatattctgtcctaaggataccgcatctggt 1797

Score = 61.9 bits (31), Expect = 2e-07
Identities = 73/87 (83%)
Strand = Plus / Plus

Query: 208 ttccatttgcaggcccttaacccaactgaacttgaatttccattggagcatatc 267
|||||
Sbjct: 4235 ttccatttgcaggcccttaacccaactgaacttgaatttccattggagcatatc 4294

Query: 268 tgaactatgaatgcgcgccttggtatt 294
|||||
Sbjct: 4295 tgaactatgaatgcgcgccttggtatt 4321

>GSEQ.ABA91636 Human C3B/C4B receptor CRL (complement receptor type
1) cDNA.
Length = 6951

Score = 599 bits (302), Expect = e-169

Identities = 350/366 (95%)
Strand = Plus / Plus

Query: 185 tcaatgcatgctccggaatgcttccatcttgcaggccctcaacccaactatgacct 244
|||||
Sbjct: 150 tcaatgcaatgcccagaatgcttccatcttgcaggccctcaacccaactatgacct 209

Query: 245 tgaattcccatggagacatatctgaactatgaatgccccttggttatctccggaagcc 304
|||||
Sbjct: 210 tgaattcccatggagacatatctgaactatgaatgccccttggttatctccggaagcc 269

Query: 305 gtcttcatcatctgcccataaaactcagcttggacaagctctaaggaacagtgcaaacg 364
|||||
Sbjct: 270 gtcttcatcatctgcccataaaactcagcttggacttggcttaaggaacagtgcaaacg 329

Query: 365 taatcatgctcgttaatcctcctcagatccttgatgcatgacacagtgatccaagaacat 424
|||||
Sbjct: 330 taatcatgctcgttaatcctcctcagatccttgatgcatgacacagtgatccaagaacat 389

Query: 425 ccagctcggatcccaaatataatctctgtcctaaaggataccgacatctgttccctc 484
|||||
Sbjct: 390 ccagctcggatcccaaatataatctctgtcctaaaggataccgacatctgttccctc 449

Query: 485 gtctgcacacatgacatcatctcaggaacacactgctcatcttgatataaacaacctgttg 544
|||||
Sbjct: 450 gtctgcacacatgacatcatctcaggaacacactgctcatcttgatataaacaacctgttg 509

Query: 545 tgacag 550
|||||
Sbjct: 510 tgacag 515

Score = 97.6 bits (49), Expect = 3e-18
Identities = 130/157 (82%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgctgtaactctccagatccctgtgaatgcatggcacatgfatcaaa 419
|||||
Sbjct: 3025 aaacgtaaatcatgctgtaactctccagatccctgtgaatgcatggcacatgfatcaaa 3084

Query: 420 gacatccagttcggatcccaaatataatctctgtcctaaagatbaacgacatctgtg 479
|||||
Sbjct: 3085 gacatccagttcggatcccaaatataatctctgtcctaaagatbaacgacatctgtg 3144

Query: 480 tccctgctgccaatgcatcatctcaggaacactg 516
|||||
Sbjct: 3145 cactcatcgtcgaatgfatcctctcaggaacactg 3181

Score = 95.6 bits (48), Expect = 1e-17
Identities = 102/120 (85%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgctgtaactctccagatccctgtgaatgcatggcacatgfatcaaa 419

|||||
Sbjct: 1675 aaacgtaaatcatgtaaaactcctcagatccctggaatgcatgctgfatcatcaaa 1734

Query: 420 gacatccagttcggatcccaaatataatctctgtcctaaagatbaacgacatctgtg 479
|||||
Sbjct: 1735 gacatccagttcggatcccaaatataatctctgtcctaaagatbaacgacatctgtg 1794

Score = 61.9 bits (31), Expect = 2e-07
Identities = 73/87 (83%)
Strand = Plus / Plus

Query: 208 ttccatttgcaggcctcaacccaactaactgfatcttgaatttcccatggaacatc 267
|||||
Sbjct: 4232 ttccatttgcaggcctcaacccaactaactaactgfatcttgaatttcccatggaacatc 4291

Query: 268 tgaactaagaatgcccgccttggttact 294
|||||
Sbjct: 4292 tgaactaagaatgcccgccttggttact 4318

>GSE01ABX84738 Human cDNA differentially expressed in granulocytic
cells #1309.
Length = 6951

Score = 599 bits (302), Expect = e-169
Identities = 350/366 (95%)
Strand = Plus / Plus

Query: 185 tcaatgcaatgctccggaatgcttccatcttgcaggccctcaacccaactatgacct 244
|||||
Sbjct: 150 tcaatgcaatgctccggaatgcttccatcttgcaggccctcaacccaactatgacct 209

Query: 245 tgaattcccatggagacatatctgaactatgaatgccccttggttatctccggaagcc 304
|||||
Sbjct: 210 tgaattcccatggagacatatctgaactatgaatgccccttggttatctccggaagcc 269

Query: 305 gtcttcatcatctgcccataaaactcagcttggacaagctctaaggaacagtgcaaacg 364
|||||
Sbjct: 270 gtcttcatcatctgcccataaaactcagcttggacttggcttaaggaacagtgcaaacg 329

Query: 365 taatcatgctcgttaatcctcctcagatccctgtgaatgcatggcacatgfatcaaaagacat 424
|||||
Sbjct: 330 taatcatgctcgttaatcctcctcagatccctgtgaatgcatggcacatgfatcaaaagacat 389

Query: 425 ccagctcggatcccaaatataatctctgtcctaaagatbaacgacatctgttccctc 484
|||||
Sbjct: 390 ccagctcggatcccaaatataatctctgtcctaaagatbaacgacatctgttccctc 449

Query: 485 gtctgcacacatgacatcatctcaggaacacactgctcatcttgatataaacaacctgttg 544
|||||
Sbjct: 450 gtctgcacacatgacatcatctcaggaacacactgctcatcttgatataaacaacctgttg 509

Query: 545 tgacag 550
|||||

Sbjct: 510 tgacag 515

Score = 97.6 bits (49), Expect = 3e-18
Identities = 130/157 (82%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgctcgttaatccctccagatccctgtgaatggcatggcacatgtaacaa 419

Sbjct: 3025 aaacgtaaatcatgtaaaactccctccagatccagtgaaatggcatgggtgacatgtaacaa 3084

Query: 420 gacatccagttcggatcccaatlaatatcttgcctaaaggataccgacatctgtgt 479

Sbjct: 3085 gacatccagttcggatcccaatlaatatcttgcctaaaggataccgacatctgtgt 3144

Query: 480 tccctgcctgcacatgcatcatcctcaggaacacatcg 516

Sbjct: 3145 cactcatctgctgaaatgtaatcctcctcaggaacacatcg 3181

Score = 95.6 bits (48), Expect = 1e-17
Identities = 102/120 (85%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgctcgttaatccctccagatccctgtgaatggcatggcacatgtaacaa 419

Sbjct: 1675 aaacgtaaatcatgtaaaactccctccagatccagtgaaatggcatgggtgacatgtaacaa 1734

Query: 420 gacatccagttcggatcccaatlaatatcttgcctaaaggataccgacatctgtgt 479

Sbjct: 1735 gacatccagttcggatcccaatlaatatcttgcctaaaggataccgacatctgtgt 1794

Score = 61.9 bits (31), Expect = 2e-07
Identities = 73/87 (83%)
Strand = Plus / Plus

Query: 208 ttccatttgcagagcctacacaaatcaatgaatcttgagtttcccatgggacatc 267

Sbjct: 4232 ttccatttgcagagcctacacaaatcaatgaatcttgagtttcccatgggacatc 4291

Query: 268 tgaactaagaatgcgccttggtta 294

Sbjct: 4292 tgaattatgaatgcgccttggtta 4318

>GSE01A158380 Human polynucleotide SEQ ID NO 583.
Length = 7313

Score = 599 bits (302), Expect = e-169
Identities = 350/366 (95%)
Strand = Plus / Plus

Query: 185 tcaatgcaatgtcccggaatggtctccatttgcagggcctaccacaaactaactgaatgact 244

Sbjct: 150 tcaatgcaatgcccagaaatggtctccatttgcagggcctaccacaaactaactgaatgact 209

Query: 245 tgaatttcccatggagacatactgacatgaatgcgccttgatctccggaaagacc 304
Sbjct: 210 tgaatttcccatggagacatactgacatgaatgcgccttgatctccggaaagacc 269

Query: 305 gtcttcatactctgcctaaanaaactcagcttggaagaatgctgaaggacaagtgcgaacg 364
Sbjct: 270 gtcttcatactctgcctaaanaaactcagcttggaatgctgaaggacaagtgcgaacg 329

Query: 365 taatcatatgctgaatcctccagatcctgtgaatgcatggacatgataatgaagaacat 424

Sbjct: 330 taatcatatgctgaatcctccagatcctgtgaatgcatggatgcatgataatgaagaacat 389

Query: 425 ccagttcggatcccaatlaatatcttgcctaaaggataccgacatctgtgtcctc 484

Sbjct: 390 ccagttcggatcccaatlaatatcttgcctaaaggataccgacatctgtgtcctc 449

Query: 485 gtctgcacatgcatcatcctcaggaacacatgctcatctggatataaacaacatctgtg 544

Sbjct: 450 gtctgcacatgcatcatcctcaggaacacatgctcatctggatataaacaacatctgtg 509

Query: 545 tgacag 550

Sbjct: 510 tgacag 515

Score = 97.6 bits (49), Expect = 3e-18
Identities = 130/157 (82%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgctcgttaatccctccagatccctgtgaatggcatggcacatgtaacaa 419

Sbjct: 3025 aaacgtaaatcatgtaaaactccctccagatccagtgaaatggcatgggtgacatgtaacaa 3084

Query: 420 gacatccagttcggatcccaatlaatatcttgcctaaaggataccgacatctgtgt 479

Sbjct: 3085 gacatccagttcggatcccaatlaatatcttgcctaaaggataccgacatctgtgt 3144

Query: 480 tccctgcctgcacatgcatcatcctcaggaacacatcg 516

Sbjct: 3145 cactcatctgctgaaatgtaatcctcctcaggaacacatcg 3181

Score = 95.6 bits (48), Expect = 1e-17
Identities = 102/120 (85%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgctcgttaatccctccagatccctgtgaatggcatggcacatgtaacaa 419

Sbjct: 1675 aaacgtaaatcatgtaaaactccctccagatccagtgaaatggcatgggtgacatgtaacaa 1734

Query: 420 gacatccagttcggatcccaatlaatatcttgcctaaaggataccgacatctgtgt 479

Sbjct: 1735 gacatccagttcggatcccaatlaatatcttgcctaaaggataccgacatctgtgt 1794

Score = 61.9 bits (31), Expect = 2e-07
Identities = 73/87 (83%)
Strand = Plus / Plus

Query: 208 ttccatttgcagcgcctaccacccaactgaatgaatttgcattcccatcggacatc 267
|||||
Sbjct: 4232 ttccatttgcagcgcctaccacccaactgaatgaatttgcattcccatcggacatcct 4291

Query: 268 tgaactaagaatgcgcgccttgattc 294
|||||
Sbjct: 4292 tgaactaagaatgcgcgccttgattc 4318

>GSEQ:AA238150 Human C3b/C4b receptor (CRI) protein encoding DNA.
Length = 6951

Score = 599 bits (302), Expect = e-169
Identities = 350/366 (95%)
Strand = Plus / Plus

Query: 185 tcaatgaatgtcccggaatgtcttccatttgcagggcctaccacctaactgaatgact 244
|||||
Sbjct: 150 tcaatgaatgtcccggaatgtcttccatttgcagggcctaccacctaactgaatgact 209

Query: 245 tgaatttcccatgtggacatactgaactatgaatgcgcgccttgatttccggaagacc 304
|||||
Sbjct: 210 tgaatttcccatgtggacatactgaactatgaatgcgcgccttgatttccggaagacc 269

Query: 305 gtcttcatactgccttaaaaaactcagtcctggaacagtgctaaaggaacgtgcaaacg 364
|||||
Sbjct: 270 gtcttcatactgccttaaaaaactcagtcctggaacagtgctaaaggaagggtcgagcag 329

Query: 365 taatcatgtcgttaactctccagatcctcgtgaatgtgcacatgcatccaagacat 424
|||||
Sbjct: 330 taatcatgtcgttaactctccagatcctcgtgaatgtgcacatgcatccaagacat 389

Query: 425 ccagtcggaatcccaaatlaatatctgtcctaaaggaataccgaatcattggtccctc 484
|||||
Sbjct: 390 ccagtcggaatcccaaatlaatatctgtcctaaaggaataccgaatcattggtccctc 449

Query: 485 gtctgcacatgcatactccaggaacacgtgcatttgggataataaaccctgtttg 544
|||||
Sbjct: 450 gtctgcacatgcatactccaggaacacgtgcatttgggataataaaccctcatttg 509

Query: 545 tgacag 550
|||||
Sbjct: 510 tgacag 515

Score = 97.6 bits (49), Expect = 3e-18
Identities = 130/157 (82%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgtcgttaatcctccagatcctgtgaatgcatggcacatgtgatacaaa 419

|||||
Sbjct: 3025 aaacgtaaatcatgttaaaacccctccagatccagtgaaatgcatggtcgtgataca 3084

Query: 420 gacatccagttccggatcccaatlaatatctgtcctaaaggaatccgactcattggt 479
|||||
Sbjct: 3085 gacatccagttccggatcccaatlaatatctgtcctaaaggaatccgactcattggt 3144

Query: 480 tccctgcctccacatgcatcatcctcaggcaacag 516
|||||
Sbjct: 3145 cactcatctgtcgtgaatgatactcctccaggcaatcactg 3181

Score = 95.6 bits (48), Expect = 1e-17
Identities = 102/120 (85%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgtcgttaatcctccagatccctggaatgcatggtacatgtgataca 419
|||||
Sbjct: 1675 aaacgtaaatcatgttaaaacccctccagatccagtgaaatgcatggtacatgtgataca 1734

Query: 420 gacatccagttccggatcccaatlaatatctgtcctaaaggaatccgactcattggt 479
|||||
Sbjct: 1735 gacatccagttccggatcccaatlaatatctgtcctaaaggaatccgactcattggt 1794

Score = 61.9 bits (31), Expect = 2e-07
Identities = 73/87 (83%)
Strand = Plus / Plus

Query: 208 ttccatttgcagcgcctaccacccaactgaatgaatttgcattcccatcggacatc 267
|||||
Sbjct: 4232 ttccatttgcagcgcctaccacccaactgaatgaatttgcattcccatcggacatc 4291

Query: 268 tgaactaagaatgcgcgccttgattc 294
|||||
Sbjct: 4292 tgaactaagaatgcgcgccttgattc 4318

>GSEQ:AA011642 Entire human complement type 1 receptor coding region.
Length = 6951

Score = 599 bits (302), Expect = e-169
Identities = 350/366 (95%)
Strand = Plus / Plus

Query: 185 tcaatgaatgtcccggaatgtcttccatttgcagggcctaccacccaactgaatgact 244
|||||
Sbjct: 150 tcaatgaatgtcccggaatgtcttccatttgcagggcctaccacccaactgaatgact 209

Query: 245 tgaatttcccatgtggacatcatcgtgaatgaatgcgcgccttgatttccggaagacc 304
|||||
Sbjct: 210 tgaatttcccatgtggacatcatcgtgaatgaatgcgcgccttgatttccggaagacc 269

Query: 305 gtcttcatactgccttaaaaaactcagtcctggaacagtgctaaaggaacgtgcaaacg 364
|||||

Sbjct: 270 gttttctatcatctctgcttaaaaaactcagctcgtgactggtgcttaaggacaggtgcagacg 329

Query: 365 taatcatgtctgtaattccctccagatccttgtaatggacatgacatgtgataaagacat 424
|||||
Sbjct: 330 taatcatgtctgtaattccctccagatccttgtaatggacatgtgataaagacat 389

Query: 425 ccagctcggatcccaaatataatctctgtccctaaaggataccgactcatgtgtcttc 484
|||||
Sbjct: 390 ccagctcggatcccaaatataatctctgtccctaaaggataccgactcatgtgtcttc 449

Query: 485 gtctgcacatgcatcatcttcacggcaacactgtcatcttggaataaaccactgtttcg 544
|||||
Sbjct: 450 gtctgcacatgcatcatcttcacggcaacactgtcatcttggaataaaccactatttg 509

Query: 545 tgacag 550
|||||
Sbjct: 510 tgacag 515

Score = 97.6 bits (49), Expect = 3e-18
Identities = 130/157 (82%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgtcgttaattccctccagatccttgtaatggacatgacatgtatcaaa 419
|||||
Sbjct: 3025 aaacgtaaatcatgttaaaattccctccagatccttgtaatggacatggttgatctaca 3084

Query: 420 gacatccagcttggaatcccaaatataatctctgtccctaaaggataccgactcatgtgt 479
|||||
Sbjct: 3085 gacatccagcttggaatcccaaatataatctctgtccctaaaggataccgactcatgtgt 3144

Query: 480 tccctcgtcgcacatgcatcatcttcacggcaacactgtcatcttggaataaaccactgtttcg 516
|||||
Sbjct: 3145 cactcatcgtcgttaattccctccagatccttggaataaaccactgtttcg 3181

Score = 95.6 bits (48), Expect = 1e-17
Identities = 102/120 (85%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgtcgttaattccctccagatccttgtaatggacatgacatgtatcaaa 419
|||||
Sbjct: 1675 aaacgtaaatcatgttaaaattccctccagatccttgtaatggacatggttgatctaca 1734

Query: 420 gacatccagcttggaatcccaaatataatctctgtccctaaaggataccgactcatgtgt 479
|||||
Sbjct: 1735 gacatccagcttggaatcccaaatataatctctgtccctaaaggataccgactcatgtgt 1794

Score = 61.9 bits (31), Expect = 2e-07
Identities = 73/87 (83%)
Strand = Plus / Plus

Query: 208 ttccatttgcagagccctacccaactcatgtacttgatttgcatttccatttggacatacc 267
|||||
|||||

Sbjct: 4232 ttccatttgcagagccctacccaactcatgtacttgatttgcatttccatttggacatacc 4291

Query: 268 tgaactatgaatgcgcgcctcgttact 294
|||||
Sbjct: 4292 tgaactatgaatgcgcgcctcgttact 4318

>GSEQ:AM91477 CRL protein DNA.
Length = 6951

Score = 599 bits (302), Expect = e-169
Identities = 350/366 (95%)
Strand = Plus / Plus

Query: 185 tcaatgcaatgtcccggaatggtctccatttgcaggccttaaccaacttaactgatatctt 244
|||||
Sbjct: 150 tcaatgcaatgtcccggaatggtctccatttgcaggccttaaccaacttaactgatatctt 209

Query: 245 tgaatttcccatgtggacatctcgaactatgaatgcgcgcctcgttattcccgagaacc 304
|||||
Sbjct: 210 tgaatttcccatgtggacatctcgaactatgaatgcgcgcctcgttattcccgagaacc 269

Query: 305 gttttctatcatctctgcttaaaaaactcagctcgtgacaagtgtgctaaggacaaagtgcacg 364
|||||
Sbjct: 270 gttttctatcatctctgcttaaaaaactcagctcgtgacaagtgtgctaaggacaaagtgcacg 329

Query: 365 taatcatgtcgttaattccctccagatccttgtaatggacatgacatgtatcaaaagacat 424
|||||
Sbjct: 330 taatcatgtcgttaattccctccagatccttgtaatggacatgacatgtatcaaaagacat 389

Query: 425 ccagctcggatcccaaatataatctctgtccctaaaggataccgactcatgtgtcttc 484
|||||
Sbjct: 390 ccagctcggatcccaaatataatctctgtccctaaaggataccgactcatgtgtcttc 449

Query: 485 gtctgcacatgcatcatcttcacggcaacactgtcatcttggaataaaccactgtttcg 544
|||||
Sbjct: 450 gtctgcacatgcatcatcttcacggcaacactgtcatcttggaataaaccactatttg 509

Query: 545 tgacag 550
|||||
Sbjct: 510 tgacag 515

Score = 97.6 bits (49), Expect = 3e-18
Identities = 130/157 (82%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgtcgttaattccctccagatccttgtaatggacatgacatgtatcaaa 419
|||||
Sbjct: 3025 aaacgtaaatcatgttaaaattccctccagatccttgtaatggacatggttgatctaca 3084

Query: 420 gacatccagcttggaatcccaaatataatctctgtccctaaaggataccgactcatgtgt 479
|||||
Sbjct: 3085 gacatccagcttggaatcccaaatataatctctgtccctaaaggataccgactcatgtgt 3144

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

```

Query: 480      tctctgctctgcacatgcatactctcaggaacactg 516
              ||| ||||| ||| ||| ||||| |||
Sbjct: 3145     caatcatctctgatgatgatctctctcaggaacactg 3181

```

Score = 95.6 bits (48), Expect = 1e-17
Identities = 102/120 (85%)
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgtcgttaatccctccagatctctgtgaatgcgatggcaactgttattcaa 419
|||||
Sbjct: 1675 aaacgtaaatcatgttaaaactctctccaatactcaggtagatgcgatgttgcatgtgaccaca 1734

```

Query: 420      gcatccagcttcgatcccaatcaataatctctgtccctaaagatccgacttatgt 479
               |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct: 1735      gcatccagcttcgatccagaatcaactatctctgtactacagggcacgcgacttatgt 1794

```

Score = 61.9 bits (31), Expect = 2e-07
Identities = 73/87 (83%)
Strand = Plus / Plus

```

Query: 208      ttcacattgcagcagcctaccacctaactgatacctttagttcccatcgggacataac 267
                |||||
Sbjct: 4232      ttcacattgcagcagcctaccacctaactgatacctttagttcccatcgggacatcct 4291

```

```

Query: 268      tgaactatgaatgcgcctggtatt 294
               ||| ||||| ||| ||| |||
Sbjct: 4292      tgaattatgaatgcgcctcctgggtatt 4318

```

Database: Current.Geneseq.NA.fasta
Posted date: Apr 14, 2003 11:38 AM
Number of letters in database: 1,289,285,926
Number of sequences in database: 2,461,325

Lambda	K	H
1.37	0.711	1.31

Gapped	K	H
Lambda	0.711	1.31
1.37		

```

Matrix: Blastn Matrix: 1 - 5 Extension: 2
Gap Penalties: Existence: -3
Number of Hits to DB: 466016
Number of Sequences: 2461325
Number of extensions: 466016
Number of successful extensions: 32593
Number of sequences better than 10.0: 91
length of query: 627
length of database: 1,289,285,926
effective HSP length: 20
effective length of query: 607
effective length of database: 1,240,059,426
effective search space: 752716071582
effective search space used: 752716071582
T: 0

```

```
X1: 6 (11.9 bits)
X2: 10 (19.8 bits)
S1: 12 (24.3 bits)
```

Graphical Viewer...

Submit sequences to:

Submit

Reset

